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Nagase, T., Ishikawa, K., Nakajima, D., Ohira, M., Seki, N., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O. Preddiction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro
DNA Res. 4 (2), 141-150 (1997)
                                                                                                                                                                                                                                                                                                                                                      CQ589124 Sequence
AC020539 Drosophil
AC01021 Drosophil
AC010037 Drosophil
AK114825 Ciona int
AK113004 Ciona int
AK13004 Ciona int
AK133465 Gallus ga
BC007645 Homo sapi
AC125966 Rattus no
BD148725 Primer fo
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Chara,O., Nagase,T., Kikuno,R. and Nomura,N.
Direct Submission
Direct Submission
Submitted (28-MX-1997) Osamu Ohara, Kazusa DNA Research Institute, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
Location/Qualifiers
1. 6791
                                                                  CQ727300 Sequence
BD160555 Primer fo
AX883831 Sequence
AX024287 Homo sapi
BB057820 Secreted
BD187820 Secreted
BD187820 Secreted
BD18795 Primer fo
AX879698 Sequence
BD187975 Primer fo
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BT010098 Drosophil
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AC012648 Drosophil
AC023733 Drosophil
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Gallus ga
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-MODEL=frame+ D2n.model -DEV=xlp
-D6-fcgm2 1/05PT0 5pool D/010/064390/runat 12102005 110203 22329/app_guery.fasta_1.1223
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINWATCH=0.1 -LÖOPCL=0 -LÖOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LLST=45
-DOCALIGN=200 -THR SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-UOTFWM=pto -NORM=ext - HEAPSIZE=500 -MINIENB=0 -MAXIEN=2000000000
-USER=USIO764390_@CGN 1 1.6626 @runat 12102005 110203 22329 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPEJOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPEJOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                      nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTGTGACCTGTCCAGCTGTGACCTGGCCTGGTGGTTCGAGGGCCCGCTGCTACCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerCysProHisLysGluAsnCysGluProLysLysMetGlyProIleArgSerTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTTTGTGCTCCGGCCTGTTCAGAGGCCTGCACAGCTGCTGGACTATGGGGACATGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaArgLysGlnCysSerGluGlyArgThrTyrSerAsnAlaValIleSerProAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrPheValleuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuVa1
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                                                                                                                                                                                                        not identified
                                                                                                              plus"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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5574.00
99.72%
99.72%
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Best Local Similarity:
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DB:
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ThrvalLysGluLeuThrvalSerAlaGlyAspAsnLeuIleIleThrLeuProAspAsn 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 AlaAlaProSerGluSerThrProSerGluLeuProIleSerProThrThrAlaProArg 330
                                                                                                                                                                          ArgGluLeuGluLysAspLeuLeuGlnProSerGlyLysGlnGluProArgGlySerAla 180
                                                                                                                                                                                                                                            GluTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsn---SerSerVal 199
                                                                                                                                                                                                                                                                                                                                        GGAGACAACTCAGCTGCATGGAGAAGCTGCAGGATCCCACGCCCCACCACTGGAC 914
                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgSerValLeuLeuProLeuProThrThrPro---SerSerGlyGluValLeuGluLys 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:::
| GAAGAGACTITACAGCTCCAAGAACAACAGCAATAGCTCTGGAAAAGAGGTTCCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 GluValGluLeuLysAlaPheValAlaProAlaProProValGluThrThrTyrAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluTrpAsnLeulleSerHisProThrAspTyrGlnGlyGlulleLysGlnGlyHisLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1095 cerrecearaareerrecerrecereceredagrerageeeageeadagaaae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGAGCAGCTGCAGGCCCTGAATGAGTCGACTTGGTCCCCTACACCCGGGCACTCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGluAsnAlaPheGlyGluGlyPheValAsnValThrValLysProAlaArgArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnLeuProProValAlaValValSerProGlnLeuGlnGluLeuThrLeuProLeuThr
Leu***PheLeuGlyLysAspTrpGlyLeuGluGluMetSerGluTyr***AspAspTyr
                                                                                                                                -----GluLeuHisTyrLeuAsnGluSerAlaSerThrProAlaProLysLeuProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnThrLeuAsnLeuSerGlnLeuSerValGlyLeuTyrValPheLysValThrValSer
                                                LeuAsnArgGlySerProSerGlyIleTrpGlyAspSerProGluAspIleArgLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLysAlaSerGlnLeuGlnGluGlnSerSerAsnSerSerGlyLysGluValLeuMet
                                                                                                                                                                                                                                                                                                          GlyAspSerProAlaValProAlaGluThrGlnGlnAspPro-------
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FYDLERGLIQPSNQQPPRGGARYPWSLLPENDSGGFNATATGDNSAAMERLQDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                       GKEVPNPSHNPSPASLESSPATTEKNSNFTVTPRSRKHSTFTFFTSTVITGLTPPPNP
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LALTUTLTGAVSWLCI CCCRRKRTKI RKKTYVI LLDSMDEQBRMELRPYGTKHRS
TEHNSSLMYSSEFERSQDVTLFSRERMERGYLKGSLNGCARNGYSFGYYSKDR*
                                                                                                                                                                                                                                                                                                                                                                                                         HPLDQEQLQALNESTWSPTPGHSSISSVWPSSASPLPTEEGLEGEETLQLQEQPSNSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaArgLysGlnCysSerGluGlyArgThrTyrSerAsnAlaValIleSerProAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTGTGACTTGCTCACCTGTGACCTGGTGGTTTGAGGGCAGCTGCTATCTGGTG
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820
91
1160
111
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Matches:
Conservative:
Mismatches:
Indels:
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1. .4971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-764-390-3 (1-1072) x AK122246 (1-4971)
                  Location/Qualifiers
   sequencing
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4255.50
84.20%
75.79%
76.26%
     one
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Best Local Similarity:
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Pred. No.:
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                  FEATURES
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SerGluPheAspSerAspGlnAspThrIlePheSerArgGluLysMetGluArgGlyAsn 1050
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TCTGAGTTTGAAAGCGACCAGGACACGCTATTCAGCCGAGAGAGGATGGAGAGGAGGAGGAGTC 3431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProLysValSerMetAsnGlySerIleArgAsnGlyAlaSerPheSerTyrCysSerLys 1070
                                                                                                                                                                                                                                 3072 ATCTGCTCCCAGCTGTGGATGGAGAACCTCATACAGCGGTACATGTGGGATGGAGAGAG 3131
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                                                                                                                                                                         AsnCysGluTrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThr
                                                                                                                                                                                                                                                                       3132 AACTGTGAGTGGAGTGTATTCTATGTGGCAGCTCTGGCATTGACACTAACACTAACT
                                                                                                                                                                                                                                                                                                     GlyGlyPheThrTrpLeuCysIleCysCySCySLySArgGlnLysArgThrLySIleArg
                                                                                                                                                                                                                                                                                                                 ProLysTyrGlylleLysHisArgSerThrGluHisAsnSerSerLeuMetValSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                   CCCAAGTACGGTATCAAGCACAGGAGCACGGAGCACAACTCCAGTCTGATGGTCGGAG
                                                               871 ValGlnSerArgProPheLysValLeuLysAlaAlaGluValAlaArgAsnLeuHis
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                                                                                                                                                      2952 AAGCGCCTTTCCAAGGAGAAGAGGAGCTTTCCTGCTTTTCAAGGTCTTGAGGGTAGACACA
                                                                                                                                                                                                                 | IleCysSerHisLeuTrpMetGluAsnLeuIleGlnArglyrIleTrpAspGlyGluSer
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                                                   AsplleLysValGlnLysIleArgAlaHisSerAspLeuSerThrValIleValPheTyr
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03-FEB-2004 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses Homo sapiens (human) Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. PAT pg. 3, buil

841 ACCACTGCTCCCAGGACA	ThrThrTyrAsnTyrGluTrpAsnLeulleSerHisProThrAspTyrGlnGlyGlulle 3	LysvalThrvalSerSerGluAsnAlaPheGlyGluGlyPheValAsnValThrValLys 4	4 4	466 ValSerTyrHisTrpGluGluIleAsnGlyProPhelleGluGluLysThrSerValAsp 485	ThrAspSerAspGlyAlaThrAsnSerThrThrAlaAlaLeuIleValAsnAsnAsnAlaVal 52	526 ApTyrEroProValAlaAsmAlaGlyProAsmHisThrIleThrLeuEroGlnAsnSer 545		1317	626 ValAlaValAlaGlyProAsplysGluLeullePheProValGluSerAlaThrLeuAsp 645	685 151 705 157
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/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	ignment Scores: 8 54e-212 8d. No.: 4092.00 rcent Similarity: 80.34\$ 8t Local Similarity: 973.33\$ ery Match: 6	US-10-764-390-3 (1-1072) x CQ726592 (1-2433)  QY		106 ProvalGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMetLeuAsnArgGlySer	Db         241 cccrcccccrrccccccrccccccccccccccccccc	Oy         166 AspLeuLeudInProSerdlyLysGInGluProArgGlySerAlaGluTyrThrAspTrp 185           Db		226 AlabrolysLeuProgluArgSerValLeuLeuProLeuProThrThrProSerSerGly	Db 601 GAGGTGTTGGAGAAAGACTTCTCAGGTCCAGGAACAATCCAGCAACAACCAGCTCTGGA 660  Oy 266 LysGluValLeuMetProSerHisSerLeuProProAlaSerLeuGluLeuSerSerVal 285	Db 721 ACCGTGGAGAAAGCCCAGTGTTTTTTTTTTTTTTTTTTT

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Mus musculus (Nouse Modata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Stiurognathi; Muridae; Murinae; Mus. Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Strausberg; R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Colline, F. S., Wagner, L., Shemmen, C. M., Schuler, G. D., Altschul, S. F., Zoeverg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Morce, T. , Wax, S. I., Wang, J., Haich, F., Stapleron, M., Soares, M., B., Bandldo, M.F., Casavant, T. L., Scheetz, T. E., Brownstein, M.J., Usdin, T. B., Toshiyuki, S., Carninci, P., Frange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., McKernan, K. J., Mullahy, S. J., Bosak, S. A., McEwan, P. J., McKernan, R. J., Mallek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Sodergren, E. J., Luy, X., Gibbs, R. A., Sanchez, A., Whiting, M., Sodergren, E. J., Lu, X., Gibbs, R. A., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodrigues, S., McKayn, M. C., Scheutz, J., Myers, R. M., Schein, J. B., Jones, S. J. and Marra, M. A., Schein, J. B., Jones, S. J. and Marra, M. A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23956263.
Location/Qualifiers
                                      BC028869 4379 bp mRNA linear ROD 29-JUN-2004
Mus musculus expressed sequence AU040320, mRNA (CDNA clone
MGC:28660 IMAGE:4235813), complete cds.
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Submitted (01-MR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/tisnue type="Kidney, normal. 5 month old male mouse."
/clone lib="NCI CGAP Kid14"
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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/organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                    ArgHisValLeuValLeuProAsnAsnSerIleThrLeuAspGlySerArgSerThrAsp
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pseraspGiyAlaThrAsnSerThrThrAlaAlaLeuIleValAsnAsnAsuTyaJAspTy CTCTGACGGGCTACCAACTCCACCCCGCAACCTGACTGTGACTAAAGCTGGACTA  CTCTGACGGGCCTACCAACTCCACCCCCCCACCAACTGACCTGACCTACAACTCGACCTACCCTCCACAACTCGACCAACTGACCTGCACCTCCACAACTCGACCTCCCCCCCC	2444 GAATCACTCTGACCACCACCACTGTCCTTCCTCCTCGGTGGAGGGGACCTACAC 2503  787 rPheHisLeuArgValThrAspSerGlnGlyAlaSerAspThrAspThrAlaThrValG1 807  2504 GTTCACCTGAAAGTGACAAAGGGCGAGGACGACACAGACGACGACGACGACGAGTGGA 2563  807 uValGlnProAspProArgLy8SerGlyLeuValGluLeuThrLeuGlnValGlyValG1 827  807 uValGlnProAspProArgLy8SerGlyLeuValGluLeuThrLeuGlnValGlyValG1 827  807 uValGlnProAspProArgLy8SerGlyLeuValG1ULeuThrLeuGlnValGlyValG1 827  827 AGTGAACCTGACCAGGAAAAGCACCTAGTGGAGATCATCTCTGAATGTGAACGTCAG  827 GlnLeuThrGluGlnArgLy8AspThrLeuValArgGlnLeuAlaValLeuLasnVa 847

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                                                                                                                                                                                                   ----LeuValThrIleAlaGlyCys-Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 14 Row: m Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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GMCIQADCSRPQSCRAFRTHSSNSMLVFLKKFQTADDLGFLPEDDVPHLLGLGWNWAS
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GSAEVHKALTISSPLTTDLAELSGENVSVPELSELTTFPSTQVCKSSEKTQIA
GPABARSYSYATPTQASFOSTSAPYPVIKELVVSAGESVOJTLPRKNEVOLANAYVL
BPPKGSTYTYDWQLITHPRDYSGEMEGKHSQILKLSKLIPGLYFFKVIVEGQNAHGEG
VNVTVKPEPERRENFPLAIVSPROFISILSLFTTSVIDGSGSTDDKILVQYHWEELKGP
IRREKISEDTAILKSKLVPGYYTFSLTVVNSVQYHWEELKGP
REKKISEDTAILKSKLVPGYYTFSLTVVNSDGATWSTTANITVNKAVDYPPVANAG
PROVITILPQNSIILKFGNQSTDDHGITSYEWSLSPSSKGKVVEMQGVRTPTLQLSAMQE
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DDQK11SYLWEKTQGPDGVQLENANSSVATVTGLQVGTYVFTLTVKDERNLQSQSSVN
V1VKEEINKPP1AK1TGNVV1TLPTSTAELDGSKSSDDKGIVSYLWTRDEGSPAAGEV
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HBVAAMLKSELRKQKADFLIFRALEVNTVTCQLNCSDHGHCDSFTKRCICDPFWMENF
IKVQLRDGDSNCEWSVLYVIIATFVIVVALGILSWTVICCCKRQKGKPKRKSKYKILD
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SVPNGQTPLKARSPREEIL"
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                                                                                                                                                              Submitted (24-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                  Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="polycystic kidney disease 1-like, isoform a"
/protein id="AAH14530.1"
/db_xref="G1.45708393"
/db_xref="LocusID:79932"
                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
U.S.A. 99 (26), 16899-16903 (2002)
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/mol type="mRNA"
/db xref="taxon:9606"
/dbone="MGC:11173 IMAGE:3843301"
/tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIH MGC_21"
/lab host="DH10B-R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
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db_xref="LocusID:79932"
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/gene="PKD1-like"
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                                                                                                     Strausberg, R.
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| ACTGGTGGTATCTGCTGGAGAGTGTCCAGATAACCCTGCCTAAGAATGAAGTTCAATT
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717 -AGACCTGCTGTATCTTCCAGTGACCAGCAG-------
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3208 GCTGGACAGCGAT---GATGCCATCTTTACATGCCCAGACGGAGAAGGAAACTCCT 3264
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Khan,F.A., Tang,Y.T., Baughn,M.R., Lu,D.A., Yang,J., Burford,N.,
Au-Young,J. and Reddy,R.
Screted proteins
Patent: WO 0151636-A 15 19-JUL-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Allolzis 4 4000 bp mRNA linear PRI 04-NOV-2002 Homo sapiens polycystic kidney disease 1-related protein mRNA, complete cds.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 4000)
Hool,S.
Hool,D. and Hool,S.
Direct Submission
L Submitted (12-OCT-2002) Physiology, National University of
Singapore, 2 Medical Drive, Singapore 117597, Singapore
Location/Qualifiers
I. 4000
/organism="Homo sapiens"
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Novel human cDNA clones with function of inhibiting cancer cell
                                   3051 Trigaacrgraticricrigitataaaaaccaaaaa---gaaaaaccaagaaaagcaa
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Submitted (07-JUN-2000) National Laboratory For Oncogenes
Genes, Shanghai Cancer Institute, 25/In 2200 Xie-Tu Road,
200032, P.R. China
Location/Qualifiers
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Qin,W.X., Wan,D.F., Zhou,X.M., Zhang,P.P., Jiang,H.Q.,
Zhao,X.T. and Gu,J.R.
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Homo sapiens PP791 protein mRNA,
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qa	1431	CATTGCTATTGTGTCACCTCAGTTCCAGGAGATCTCTTTGCCAACCACTTCTACAGTCAT 1490
<i>ਨ</i>	454	eAspGlySerGlnSerThrAspAspThrGluleValSerTyrHisTrpGluGluIleAs 474
Db	1491	TGATGGCAGTCAAAGCACTGATGATGATAAAATCGTTCAGTACCATTGGGAAGAACTTAA 1550
ολ	474	nGlyProPhelleGluGluLysThrSerValAspSerProValLeuArgLeuSerAsnLe 494
QQ	1551	GGGCCTCTAAGAGAAGAATTTCTGAAGATACAGCCATATTAAAACTAAGTAAACT 1610
ò	494	uAspProGlyAsnTyrSerPheArgLeuThrValThrAspSerAspGlyAlaThrAsnSe 514
ДQ	1611	CGTCCCTGGGAACTACCACTTCAGCTTGACTGTAGACTCTGATGGAGCTACCAACTC 1670
Š	514	rThrThrAlaAlaLeuIleValAsnAsnAlaValAspTyrProProValAlaAsnAlaGl 534
qq	1671	TACTACTGCAAACCTGACAGTGAACAAAGCTGTGGATTACCCCCTGTGGCCAACGCAGG 1730
ò	534	YProAsnHisThrIleThrLeuProGlnAsnSerlleThrLeuAsnGlyAsnGlnSerSe         554
qq	1731	ccccaaccaagraatcaccrigccccaaaacriccaccaccrcrrrggaaaccagagcac 1790
ò	554	rAspAspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySerGluGlyLysHi 574
Op	1791	TGATGATCATGGCATCACCAGCTATGAGTGGTCACTCAGCCCAAGCAGAAGGAAAGT 1850
ò	574	BValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMetGlnGlyAs 594
οp	1851	GGTGGAGATGCAGGGTGTTAGAACACCAACCTTACAGCTCTCTGCGATGCAAGAAGGAGA 1910
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Db 3051 CTGGACTGTGATCTGTTGATAAAAGGAAAACCAGAGGAAAACCAGAGGAAAACCAGAGGAAAACCAGAGGAAAACCAGAGGAAAACCAGAGGAAAACCAGAGGAAAACCAGACGAAAACCAGAAAACCAGAAAACCAGAAAACCAGAAAACCAGAAAACCAGAAAACCAGAAAACCAGACCACACACCAC	Alignment Scores:     2.88e-113
1911	934 ysAspThrLeuValArgGlnLeuAlaValLeuLeuAsnValLeuAspSerAspIleLysV 854 2631 AGGGATGTTCGCCAGATTGGGGTCCTCCGGGGGTGCTGGATTCCGACATCATG 2690 854 alGlnLysIleArgAlaHisSerAspLeuSerThrValIleValBheTyrValGlnSerA 874 2691 TGCAAAAGATTCGCCGTACACGGAGCAGACACCCAAATGGTATTTTTGTTCAAAAGG 2750 874 rgProProPheLysValLeuLysAlaAlaGluValAlaArgAsnLeuHisMetArgLeuA 894 2751 AGCTCCCCACCAGATCTTCAAAGGCCATGAGGTGGCGAGCGA

640 GluseralaThrLeuAspGlySerSerSerSerAspAspHisGly1leValPheTyrHis 659 :::	660 TrpGluHisValArgGlyProSerAlaValGluMetGluAsnIleAspLysAlaIleAla 679 	680 ThrValThrGlyLeuGlnValGlyThrTyrHisPheArgLeuThrValLysAspGlnGln 699	71	720 ArgAlaArgAlaGlyGlyArgHisValLeuValLeuProAsnAsnSerIleThrLeuAsp 739	740 GlyserArgSerThrAspAspGlnArgIleValSerTyrLeuTrpIleArgAspGlyGln 759	760 SerProAlaAlaGlyAspVallleAspGlySerAspHisSerValAlaLeuGlnLeuThr 779	780 AsnLeuvalGluGlyvalTyrThrPheHisLeuArgValThrAspSerGlnGlyAlaSer 799	800 AspThrAspThrAlaThrValGluValGlnProAspProArgLysSerGlyLeuValGlu 819	820 LeuthrLeuGlnValGlyValGlyGlnLeuthrGluGlnArgLysAspThrLeuValArg 839 :::	840 GInLeuAlaValLeuLeuAsnValLeuAspSerAspIleLysValGInLysIleArgAla 859	860 Hisseraspleuserthrvalllevalphetyrvalginserargproprophelysval 879 ::::::::               ::	880 LeulysAlaAlaAluValAlaArgAsnLeuHisMetArgLeuSerLysGluLysAlaAsp 899	900 PheLeuLeuPheLysValLeuArgValAspThrAlaGlyCysLeuLeuLysCysSerGly 919	920 HisGlyHisCysAspProLeuThrLysArgCysIleCysSerHisLeuTrpMetGluAsn 939	940 LeulleGlnArgTyrIleTrpAspGlyGluSerAsnCys952    :::	953GluTrpSerllePheTyrValThrValLeuAlaPheThrLeuIleValLeuThr 970	971 GlyGlyPheThrTrpLeuCysIleCysCysCysCysLysArgGlnLysArgThrLysIleArg 990	
ò a	ò a	çy B	oy Od	S G	ර් යි	δ P	oy op	SP G	B &	ò q	oy B	oy G	Sy da	S G	S d	& 8	S G	È
	311	331 ThrValLysGluLeuThrValSerAlaGlyAspAsnLeulleIThrLeuProAspAsn	351 GluvalGluLeuLysAlaPhevalAlaProAlaProProValGluThrThrTyrAsnTyr 733 GAAGTTCAATTAAATGGTATGTTCTCCAAGAACCACTAAAGGAGAAACCTACAACCTACACCTAAACCCTACACCTAAACCCTAAAACCCTAAAACCCTAAAAAGAAACCCTAAAAAGAAAAAAAA	371 GlufrpasnieulleSerHisProThraspTyrGlnGlyGlulleLysGlnGlyHisLys :::          :::	391 GlnThrLeuAsnLeuSerGlnLeuSer	400 ValGlyLeuTyrValPhelysValThrValSerSerGluAsnAlaPheGlyGluGlyPhe	420 ValasnValThrValLysProAlaArgArgValAsnLeuProProValAlaValValSer	440 ProglnLeuglnGluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSer	460 ThrAspAspThrGluileValSerTyrHisTrpGluGluileAsnGlyProPheileGlu	480 GluLysThrSerValAspSerProValLeuArgLeuSerAsnLeuAspFroGlyAsnTyr	500 SerPheArgLeuThrValThrAspSerAspGlyAlaThrAsnSerThrThrAlaAlaLeu ::::	520 IleValAsnAsnAshAspTyrProProValAlaAsnAlaGlyProAshHisThrile	540 ThrLeuProGladenserIleThrLeuAsnGlyAsnGlaSerSerAspAspHisGlaIle	560 ValLeuTyrGlufTpSerLeuGlyProGlySerGluGlyLysHisValValMetGlnGly 1.00	580 ValGlnThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAspTyrThrPheGlnLeu 5	600 LygValThrAspSerSerArgGlnGlnSerThrAla***ValThrValIleValGlnPro	1513 ACAGIGACIGACACAAIAGGACAGCCACIGCTCAAGIGACIGITATIGIGCAACCCI 620 GluasnaraproprovalalaValalaGlyproasplysGluLeullePheProVal 	Db 1573 GAAAACAATAAGCCTCCTCAGGCAGATGCAGGCCCAGATAAAGAGCTGACCTTCCTGTG 1632

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CCCATTGCTATTGTGTCACGTCAGGAGATCTCTTTGCCAACCACTTCTACAGTC 302
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                                                                                                                             674 IleAspLysAlaileAlaThrValThrGlyLeuGlnValGlyThrTyrHisPheArgLeu
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                                                                               ProvalAlavalvalSerProGlnLeuGlnGluLeuThrLeuProLeuThrSerAlaLeu
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1 (bases 1 to 2796)
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full.length cDNA and use thereof HELIX RESEARCH INSTITUTE
                                    Pro-----LysTyrGlyIleLysHisArgSerThrGluHisAsnSerSerLeuMetVal 1028
                                                   17-JAN-2003
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KEIICHI NAGAI, TETSUJI OTSUKI
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Primer for synthesizing full-length CDNA and use thereof FH K
Location/Qualifiers
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JP 2002191363-A/15398
09-JUL-2002
29-JUL-2000 JP 2000280990
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI
                                                                                                                                GlyAsnProLysValSerMetAsnGlySerIleArgAsnGly 1062
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Location/Qualifiers
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Primer for synthesizing
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Homo sapiens (human)
Homo sapiens
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          Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use. Patent: EP 1074617-A 18736 07-FEB-2001; Research Association for Bittechnology (JP) Location/Qualifiers
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                              LysSerGlyLeuValGluLeuThrLeuGlnValGlyValGlyGlnLeuThrGluGlnArg
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                                                                                      AspSerGlnGlyAlaSerAspThrAspThrAlaThrValGluValGlnProAspProArg
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1563 GAGCCTCCCCCACCACATCTCAAAAGCCCACGAGGCGCGACCCACACACA	Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takabashi-Fuji, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemcto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Pujiwara, T., Ono, T., Yamada, K., Fujii, Y., Cozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
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Birect Submission

Direct Submission

Birect Submission

Submitted (13-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(B-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5' & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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GMFIRQIGVLLGVLDSDIIVQKIQPYTEQSTKMVFFVQNEPPHQIFKGHEVAAMLKSE
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NCEMSVLYVIIATFVIVVALGILSWTVICCCKRQKGKPKRKSKYKILDATDQESLELK
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SITLFGNQSTDDHGITSYEWSLEPSSKGKVVEWQGVRTPTLQLSAMQEGDYTYQLTVT
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Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morlinaga, M., Saasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, X., Yada, T., Nakamura, Y., Ohara, V., Yada, T., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S. Complete sequencing and characterization of 21,243 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="cloning vector: pME18SFL3-mRNA from NT2 n
precursor cells after 2-weeks retinoic acid (RA)
induction."
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

9.74e-109 2184.50 73.14% 60.06% 39.15%

Similarity:

Best Local

Query Match: DB:

Percent Similarity:

Pred. No.:

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GCTAACAGCAGTGTTGCTACTGTGACTGGGGCTGCAAGTGGGGGACCTATGTGTTTCACCTTG 1022
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63 CTGATTACTCATCCTAGAGACTACAGTGGAAATGGAAACATTCCCAGATCTC
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LeuLysAlaPheValAlaProAlaProProValGluThrThrTyrAsnTyrGluTrpAsn
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.B., Brownstein, M.J., Gudin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Malek, J.A., Gurarane, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butfard, G.G., Blakesley, R.W., Touchman, J. W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Human and mouse cDNA sequences

12477927 12732
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Location/Qualifiers
                                                         BC031672 2743 bp mRNA linear PRI 04-JUN-2004
Homo sapiens polycystic kidney disease 1-like, mRNA (cDNA clone
IMAGE1446786), partial cds.
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Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center.
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                      Euteleostomi;
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Submitted (06-J70-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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/tissue type="Kidney, hypernephroma"
/clone_lib="NIH MGC_89"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV-SPORT6"
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/db_xref="taxon:9606"
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TITLE
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SOURCE
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ACTGTCAAAGATGAGGGAACCTGCAAAGCCCAGAGCTCTGTGAATGTCATTGTCAAAGAA 1082
                                                                                                                                                                                                                                                                                        1263 CCTATCCTTTTCTTTCAAACCTGGTTGAGGBAACCTACACTTTTCACCTGAAAGTGACC 1322
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Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 8 (2), 85-95 (2001)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
PheTyryalThrValLeuAlaPheThrLeuIleValLeuThrGlyGlyPheThrTrpLeu
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Homo sapiens mRNA for KIAA1837 protein, partial cds.
AB058740
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/organism="Homo sapiens"

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/rissue_type="brain"

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gene="XIAA1837"
/note="Start codon is not identified"
/codon_start=1</pre>
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/db_xref="G1:14017891"
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
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KPTSRAGRGPGCQSF"

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                                                                                                                                   CTGTATGAATTCAAAGTGATTGTAGAGGGTCAAAAATGCCCATGGGGAAGGCTATGTGAAC
                                                                                                                                                                                                        TTCCAGGAGATCTCTTTGCCAACCACTTCTACAGTCATTGATGGCAGTCAAAGCACTGAT
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                                                                                                                                                           ValThrValLysProAlaArgArgValAsnLeuProProValAlaValValSerProGln
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Mismatches:
Indels:
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                                                                                                                                                                                                                  Merberg, D.,
                                                                                                    PAT
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E 1 (bases 1 to 2501)

S Jacobs, K., Mccoy, J. M., Lavallie, E.R., Racie, L.A., Merbe Treacy, M., Spaulding, V. and Agostino, M.J.

Secreted proteins and polynucleotides encoding them patent. JP 2001514220-A 8 11-SEP-2001, GENETICS INSTITUTE INC PN JP 2001514520-A/8

PD 11-SEP-2001

PF 09-MAR-1998 JP 1998539683

PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA
                                                                                                                                                                                                                                                                                                                  DAVID MERBERG,
PI MAURICE TREACY, VIKKI SPAULDING, MICHABL J AGOSTINO
C12N15/12, C07K14/47, A61K38/17
CC Strandedness: Double,
CC Topology: Linear;
FH Key
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                                                                                                     702 SerSerThrSerThrLeuThrValAlaValLysLysGluAsnAsnSerProProArgAla
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                                                                                     HisValArgGlyProSerAlaValGluMetGluAsnIleAspLysAlaIleAlaThrVal
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US-10-764-390-3 5580 1 MAPPIGVLSSLLLLVTIAGC.....VSWNGSIRNGASFSYCSKDR 1072 score: Sequence: Title: Perfect

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\*geneseqp2003bs:\* A\_Geneseq\_16Dec04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp20048:\* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

		de			SOMMENTES		
Result No.	Score	Query Match	Length	DB	ID	Description	
-	5576	99.9	1072	7	ADJ69816	Adj69816 Human hea	ı nd
7	5576	99.9	1072	۵	ADR00600		4
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S	5574	6.66	1072	8	ADR00598	Adr00598 Human 254	4
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19	1451.5	26.0	1069	4	ABB63364	Abb63364 Drosophi	_
20	1440.5	25.8	685	4	AAB94231	Human	0
21	1375	24.6	711	4	ABG08994	Abg08994 Novel hum	E
22	1296.5	23.2	640	7	ADF42454	Adf42454 Human PP7	7
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ADK3 6703	AAW69431	ADK34788	ABP07182	AAB38389	ABU21703	ADQ89964	AAU05396	ADQ17316	ADC31624	ADO84848	ABB58144	ADQ89760	AA007167	ABU47253	ADC01014	AAY92718	ABG74786	ABB68397	ABB36684
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56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

mitochondrial; human; screening assay; diabetes mellitus; Huntington's disease; osteoarthritis; Lieber's hereditary optic neuropathy; LHON; mitochondrial encephalogathy lactic acidosis and stroke; MELAS; myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic. Human heat mitochondrial protein as a therapeutic target SeqID1622. ADJ69816 standard; protein; 1072 AA (first entry) 06-MAY-2004 ADJ69816; ADJ6981 

WO2003087768-A2 sapiens 23-OCT-2003 Ношо

04-APR-2003; 2003WO-US010870.

12-APR-2002; 2002US-0372843P. 17-JUN-2002; 2002US-0389987P. 20-SEP-2002; 2002US-0412418P.

(MITO-) MITOKOR. (BUCK-) BUCK INST AGE RES.

Gibson BW, Taylor SW, Zhang B, Fahy ED, Warnock DE; Ghosh SS,

Glenn GM;

WPI; 2003-845369/78.

Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.

Claim 1; SEQ ID NO 1622; 180pp; English.

This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for

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identifying proteins of the human heart mitochondrial protecome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, antischondrial anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
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Sequence 1072 AA;

ö 9 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA Gaps ; Length 1072; Indels 3; 7; Score 5576; DB Pred. No. 0; 0; Mismatches 99.9%; Query Match Best Local Similarity 99.7 Matches 1069; Conservative 유 ઠે

120 9 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 61

120 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 61

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EHSI PIPPISAAPSESTPSELPI SPTTAPRTVKELTVSAGDNI I ITLPDNEVELKAFVAP EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP 241 301 301

NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE 421 421

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VIDSSRQQSTAVVIVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN EHVRGPSAVEMENIDKAIATVTGLOVGTYHFRLTVKDOOGLSSTSTLTVAVKKENNSPPR 601 661 661 721

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ARAGGRHVLVLPINNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ 781

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VLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020 960 960 781 LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLMMENLIQRYIMDGESNCEWSIFYVT LAVLLINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT LAVLLNVLDSD1KVQK1RAHSDLSTV1VFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 1021 1021 841 901 901 196 셤 원 g 셤 ò δ ò ò

Z ADR00600 standard; protein; 1072 ADR00600; RESULT 2 ADRO0600 

(first entry) 04-NOV-2004 Human 254P1D6B v.5 protein SEQ ID NO:11.

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.5; chromosome 6.

Homo sapiens.

WO2004067716-A2.

12-AUG-2004.

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23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P.

(AGEN-) AGENSYS INC.

3 g Д. Ж Challita-Eid Jakobovits A, Perez-Villar JJ, Faris M; Raitano AB, SB,

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting protein or correspor and treating cancer.

SEQ ID NO 11; 345pp; English. Example 1; The present invention describes a 254Plb6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254Plb6B protein, or corresponds to a subsequence of the ORF, where the coule stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or consists essentially of, or consists of a peptide of eight, nine, ten, or cleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID No.3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in the specification, or a protein craw of the 42 lists of peptides, given in the specification, or a protein craw of the 42 lists of peptides, given in the specification, or a protein craw of the 42 lists of peptides, given in the specification, or a protein craw of the protein call acquence of P1; (2) a polynucleotide craw that is a full complement of the polynucleotide described above, (4) generating a mammalian immune response directed to the protein or a generating, in a sample, the presence of a 254PlD6B-related protein or

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(AGEN-) AGENSYS INC
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Adr0727 E
Adb05625 C
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Adr00726 F
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Adr00641 F
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Adr00828 Human 254 Adr00631 Human 254 Aab25603 Peptide e	Ada27075 Human nov Ade86607 Integrin Adc35432 FITC labe		Adro0747 Human 254 Adro0810 Human 254 Aap81554 Human ins Adi80581 Conjugate	Aab25607 Peptide e Ada27079 Human nov Ade86611 Integrin Abb08283 Human Gal	Abu07534 Human N-a Ade25869 Human muc
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## ALIGNMENTS

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.5; chromosome 6. 3 g Challita-Eid PM, Human 254P1D6B v.5 peptide SEQ ID NO:268 Jakobovits A, ADR00857 standard; peptide; 29 AA. 23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P Perez-Villar JJ, Faris M; (first entry) Raitano AB,

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 13; SEQ ID NO 268; 345pp; English.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to 254PID6B protein, open reading frame (ORF) sequence which encodes the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, or sessentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADRO0592, ADRO0594 or ADRO0596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein

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generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related protein or a catus of a cell that expresses a protein of P1; (7) a pharmaceutical catus of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human control of an antibody or its fragment, which is smootlonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and can be express the protein of P1; and can be used in gene thoraty. The compositions, molecules and methods are useful to treating and detecting cancer. The present sequence represents a human 254PlD6B v. 5 peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
   92, 93, 94, 95, 96, 97, 98, or 99% homologous or
                         identical to an entire amino acid sequence of P1; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4)
   is at least 90, 91,
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## Sequence 29 AA;

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Gaps
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2.8%; Score 158; DB 8; Length 29; 96.6%; Pred. No. 0.00021; ive 0; Mismatches 1; Indels
                                                                 128 GIWGDSPEDIRKDLXFLGKDWGLEEMSEY 156
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                Local Similarity 96.6
nes 28; Conservative
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ADR00851 standard; peptide; 29 AA.
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RESULT
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Human 254PlD6B v.2 peptide SEQ ID NO:262.

254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.2; chromosome 6.

Homo sapiens.

WO2004067716-A2

12-AUG-2004

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P

(AGEN-) AGENSYS INC.

g Challita-Eid PM, Jakobovits A, Perez-Villar JJ, Faris M; Kanner SB, Raitano AB,

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WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 13; SEQ ID NO 262; 345pp; English.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PID6B protein, or corresponds to a subsequence of the ORF, where the

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consists essentially of, or consists of a peptide of eight, nine, ten, or consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (91, see SEQ ID CC eleven contiguous amino acids of a protein of figure 2 (91, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in the start is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) composition a mammalian immune response directed to the protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the catture of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human cut that comprises the composition described above in a human confidence of a cell that expresses the protein of P1; (7) a pharmaceutical confidence and antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that expresses the protein of P1; and cell in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254P1D6B year is located on chromosome 6p22.
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0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 254PlD6B v.2 peptide SEQ ID NO:261.
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Perez-Villar JJ, Faris M;
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                      The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the uncleic acid open reading frame (ORF) sequence which encodes the 254P1D6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 23, 24, or 25 contiguous nucleotides in length, Also described: (1) a composition that comprises onsists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 [Pl, see SRQ ID NO:3, so or 7 ADRO0592, ADRO0595), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4)
                                                                                                                                                                                                                                                                                                                                 hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254Plo6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254Plo6B v.2 peptide, which is used in the exemplification of the present invention. The human 254Plo6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                            generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related protein or a status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a
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254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
254P1D6B v.5; chromosome 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 101; DB 94.7%; Pred. No. 1.6; iive 0; Mismatches
SEQ ID NO 261; 345pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR00856 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 WGLEEMSEYXDDYRELEKD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WGLEEMSEYADDYRELEKD 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-2004; 2004WO-US001965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JAN-2003; 2003US-0442526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kanner SB, Raitano AB, J
Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 94.7
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-580991/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-2004.
Example 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The present invention describes a 254P1D6B small interfering RNA (siRNA)

composition that comprises a double stranded siRNA that corresponds to

the nucleic acid open reading frame (ORF) sequence which encodes the

composition that corresponds to a subsequence of the ORF, where the

double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous

nucleotides in length. Also described: (1) a composition that comprises,

consists essentially of, or consists of a peptide of eight, nine, ten, or

eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID

NO:3, 5 or 7 ABN00592, ABN00594 or ABN00596, or a peptide included in

any of the 42 lists of peptides, given in the specification, or a protein

that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or

chat is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or

chat is a full complement of the polymucleotide described above; (4)

chat is a full complement of the polymucleotide described above; (4)

detecting, in a sample, the presence of a 254P1D6B-related protein or a

capania a mammalian immune response directed to the protein of a

capania of a cell that expresses a protein of P1; (7) a pharmaceutical

composition that comprises the composition described above in a human

cuit dose form; (8) an antibody or its fragment, which is monoclonal; (9)

unther domesting a marmal that produces the antibody; (10) a

charactering a marmal that produces the antibody; (10) a

charactering a marmal that produces the antibody; (10) a

charactering a marmal that produces the antibody; (10) a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254PlD6B v. 5 peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
254PlD6B siRNA composition comprising a double stranded siRNA that responds to the nucleic acid ORF sequence which encodes the 254PlD6B cain or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                               Example 13; SEQ ID NO 267; 345pp; English
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                                                                                                      protein or correspond
and treating cancer.
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nes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 6.
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Matches
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ADR00632
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The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the corresponds to a subsequence of the ORF, where the 254PlD6B protein, or corresponds to a subsequence of the ORF, where the coulectides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or consists sesentially of, or consists of a peptide of eight, nine, ten, or carry of the 42 lists of peptides, of a peptide included in any of the 42 lists of peptides, given in the specification, or a protein control to an entire amino acid sequence of P1; (2) a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide that is a full complement of the polymucleotide described above; (4) generating a mammalian immune response directed to the protein or a 254PlD6B-related polymucleotide; (6) a composition that modulates the composition that modulates the composition that comprises the composition described above in a human composition that comprises the composition described above in a human composition animal that produces the monoclonal; (9) a polymucleotide animal dose form; (8) an antibody or its fragment, which is monoclonal; (9) which are produced that produces the animal animal animal that produces the monoclonal; (1) which are produced animal that produces the monoclonal; (1) which are produced and animal animal animal that produces the monoclonal; (1) which are produced and animal animal animal that produces the monoclonal; (1) which are produced and animal animal animal that produces the monoclonal; (1) which are produced and animal animal animal that produced the produced animal animal animal that produced the produced animal animal animal animal that produced the produced animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal anim
    The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254P1D6B protein, or corresponds to a subsequence of the occess the consists acid open reading frame (ORF) sequence of the codes the consists as sentially of, or consists (1) a composition that comprises, consists essentially of, or consists (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO.3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98 homologous or that is a tleast 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98 homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) capacating a mammalian immune response directed to the protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition that modulates the capacities of a call that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human control or a confidence form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent confidence form; (8) an antibody or its fragment, which is monoclonal; (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1; (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. Cancer cells that express the protein of P1. Cancer cells that express the protein of P1. Cancer cells that express the protein of P1. Cancer cells that the composition or survival of cancer cells that cancer cells that the cancer cells that the cancer cells that th
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                                                                                                                                                                                                                                                                         New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                              Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; SEQ ID NO 43; 345pp; English.
                                                                              Jakobovits A,
                                                                              Kanner SB, Raitano AB, J
Perez-Villar JJ, Faris M;
                                                                                                                                                                                               WPI; 2004-580991/56.
(AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 AA;
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New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting

Example 13; SEQ ID NO 266; 345pp; English.

and treating cancer.

Ge ¥;

Jakobovits A, Challita-Eid PM,

Raitano AB, Ja GJJ, Faris M;

Perez-Villar JJ,

Kanner SB,

(AGEN-) AGENSYS INC.

WPI; 2004-580991/56.

23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P.

12-AUG-2004.

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hybridoma that produces the antibody; (11) delivering a cycotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254PlD6B v. 5 peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254PlD6B; small interfering RNA; siRNA; immune response;
254PlD6B-related protein; cytostatic; gene therapy; cancer; human;
                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                           8; Length 17;
                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                           1.6%; Score 90; DB 8 94.1%; Pred. No. 8.7; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human 254PlD6B v.2 peptide SEQ ID NO:260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR00849 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                        134 PEDIRKDLXFLGKDWGL 150
                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                         1 PEDIRKDLTFLGKDWGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                  Local Similarity 94.1 les 16; Conservative
                                                                                                                                                                                                                                Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR00849;
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254P1D6B related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.5; chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254PlD6B; small interfering RNA; siRNA; immune response;
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Human 254P1D6B v.5 peptide SEQ ID NO:266,

WO2004067716-A2

Ното варіепв.

04-NOV-2004 (first entry)

ADR00855;

ADR00855 standard; peptide; 17 AA.

RESULT 6

셤 ठ

ö

Gaps

Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.

30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

WO200175067-A2.

11-OCT-2001

Homo sapiens

Novel human diagnostic protein #22057.

18-FEB-2002 (first entry)

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The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the couposition that caid open reading frame (ORF) sequence which encodes the couble stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5) generating a mammalian immune response directed to the protein of P1; (5) generating a mammalian immune response directed to the protein of P1; (5) generating a mammalian immune response threat modulates the catus of a cell that expresses a protein of P1; (7) a pharmaceutical composition that composition described above; (4) a non-human transgence and an entitle of a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that produces the antibody; (11) delivering a cyctoxic agent or a diagnostic agent to a composition or survival of cancer cells that expresses the protein of P1; (12) inhibiting growth, reproduced non environment sequence represents a cuseful for treating and detecting cancer. The present sequence represents a human 254PlD6B v. 2 peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                           New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                      Ge W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%; Score 84; DB 8; Length 17;
94.1%; Pred. No. 24;
lve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                   Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; SEQ ID NO 260; 345pp; English.
                                                                                                                                                                                                                                                                                                      Jakobovits A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 GLEEMSEYXDDYRELEK 165
                                                                                                                                                                     23-JAN-2004; 2004WO-US001965.
                                                                                                                                                                                                                24-JAN-2003; 2003US-0442526P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.1%;
                                                                                                                                                                                                                                                                                                                          Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.1
Matches 16; Conservative
254PlD6B v.2; chromosome
                                                                                                                                                                                                                                                                                                      Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-580991/56.
                                                                                                                                                                                                                                                        (AGEN-) AGENSYS INC
                                                                                   WO2004067716-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 AA;
                                          Homo sapiens.
                                                                                                                            12-AUG-2004
                                                                                                                                                                                                                                                                                                      Kanner SB,
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

Ormanac RT, Liu C, WPI; 2001-639362/73

N-PSDB; AAS86253

siodiversity.

(HYSE-) HYSEQ INC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production soft of the polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the typ.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 83; DB 4; Length 19;
100.0%; Pred. No. 34;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 claim 20; SEQ ID NO 52425; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR00854 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5°;
100.08; Fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAPPTGVLSSLLLLVTIA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPPTGVLSSLLLLVTIA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR00854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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ABG22066 standard; protein; 19 AA.

RESULT 8 ABG22066 ABG22066;

1 GLEEMSEYADDYRELEK 17

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human;

Human 254P1D6B peptide SEQ ID NO:138.

(first entry)

04-NOV-2004

ADR00727;

ADR00727 standard; peptide; 9 AA.

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The present invention describes a 234Plobs small interfering WAM (SIRWA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the CS 254Plobs protein, or corresponds to subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous double stranded siRNA is 19, 20, 21, 22, 23, 24 or 25 contiguous anino acids of a peptide of eight, nine, ten, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO.3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) cantain a mammalian immune response directed to the protein or a 254PloBe-related polynucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human confinement that produces the antibody or its fragment, which is monoclonal; (9) a non-human transgent animal that expresses the protein of P1; and call that expresses the protein of P1; and contained that produces the antibody; (11) delivering a cytostic agent to a cell that expresses the protein of P1; and contained that any produced the artibody; (11) a non-human transgent to a cell that expresses the protein of P1; and contained that produces the antibody; (11) delivering a cytostic of a call that expresses the protein of P1; and contained that a contained that any produced the artibody of call that expresses the protein of P1; and contained the contained that the produced the artibody of call that expressed the protein of P1; and call that ex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes a 254P1D6B small interfering RNA (siRNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254P1D6B siRNA composition comprising a double stranded siRNA that
                                                                                                                                                254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.3; chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Challita-Eid PM,
                                                                                                254PlD6B; small interfering RNA; siRNA; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 13; SEQ ID NO 265; 345pp; English.
Human 254PlD6B v.3 peptide SEQ ID NO:265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jakobovits A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JAN-2004; 2004WO-US001965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JAN-2003; 2003US-0442526P.
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Best Local Similarity 100..
Best Local 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-580991/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                           WO2004067716-A2
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                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kanner SB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New
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New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting

Example 9; SEQ ID NO 138; 345pp; English.

and treating cancer.

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Challita-Eid PM,

Jakobovits A,

Kanner SB, Raitano AB, Perez-Villar JJ, Faris

WPI; 2004-580991/56.

(AGEN-) AGENSYS INC.

23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P

WO2004067716-A2

12-AUG-2004.

chromosome 6. Homo sapiens.

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The present invertion users a sufficion shall invertering the composition that comprises a double stranded shrNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the cursesponds to subsequence of the ORF, where the double stranded shrNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a period of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P., see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98 homologous or that encodes the protein; of eight encodes the protein; of the protein of the protein; of the protein; of the protein; of the composition composition composition and asample, the presence of a 254PD6B-related protein or a 254PD6B-related polymucleotide described above; (4) composition that comprises the composition described above in a human curit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgent canned browders the antibody; (10) a non-human transgent to a cell that expresses the protein of P1; (7) a pharmaceutical composition at that produces the antibody; (10) a non-human transgent to a cell that expresses the protein of P1; and composition at broadcast and antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of encertivity, and can be expressed the protein of encertivity, and can be composition and because the protein of encertivity, and can be composition and the protein of encertivity and can be composition and produced the acid of cancer cells that encodes the protein of encertivity, and can be composition and produced the acid of cancer cells that encodes the protein of cancer cells that encodes the protein of encodes the antibody; and can be expressed to a continuous produced the acid of cancer cells that encodes the antibody; and can be produced to the protein of enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254P1D6B peptide, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes a 254P1D6B small interfering RNA (siRNA)
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Gaps ; 0 Indels Length 9; Query Match
1.1%; Score 63; DB 8; Le
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0;

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Gaps

; 0

Indels

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100.0%; Pred.

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946 WDGESNCEW 954

RESULT 10 ADR00727

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The invention provides a method of diagnosis of tauopathies in an individual that comprises determining the ratio of phospho-tau (181)/
c total tau. Tau and phospho tau are useful as neurological markers for the manufacture of a diagnostic kit for the diagnosis of a tauopathy and/or the differential diagnostic for a tauopathy versus a non tauopathy and/or choosing the differential diagnosts of a tauopathy versus a non tauopathy. A phospho-peptide liable to form an immunological complex with monoclonal antibody HT7 and MAB AT270 comprising at least the minimal epitope of HT7 or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy and/or for the differential diagnosis of a tauopathy versus a non cauopathy. The kit is useful for the diagnosis of Alzheimer's disease, pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal dementia and/or Frontotemporal dementia and/or for neurotoxicity in patients with leukemia. The disease, stroke and/or neurotoxicity in patients with leukemia. The disease, stroke and/or neurotoxicity in patients with leukemia. The for determining the effectiveness of a treatment. The present sequence represents a phospho-peptide binding to MAbs HT7 and AT270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the ratio of phospho-tau / total tau is useful for diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease, versus a non
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tauopathy; phospho-tau (181); neurological marker; monoclonal antibody; HT7; AT270; nootropic; neuroprotective; cerobroprotective; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 61.5; DB 4; Length 34;
29.6%; Pred. No. 3.2e+03;
iive 6; Mismatches 7; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibodies HT7 and AT270 binding phospho-peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                             AAB85615 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vanderstichele H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 40; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2000; 2000EP-00870008.
27-JAN-2000; 2000US-0178391P.
22-NOV-2000; 2000EP-00870280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2001; 2001WO-EP000560
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INNO-) INNOGENETICS NV.
WPI; 2001-476242/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vanmechelen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200155725-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                  AAB85615;
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                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                           AAB8561
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The present invention describes a method for the differential diagnosis of an individual suffering from Alzheimer's disease versus an individual suffering from mercological disease involves using phospho-tau (I) as a neurological marker. Also described are: (I) a diagnostic kit for use in the differential diagnosis of an individual suffering from Alzheimer's and disease versus an individual suffering from another neurological disease; and disease versus an individual suffering from another neurological disease; and disease versus an expectation of the diagnostic kit. (I) has neuroprotective and noctropic diagnosis and in the manufacture of a diagnostic kit for the differential diagnosis of an individual suffering from Alzheimer's disease versus an individual suffering from another neurological disease such as dementics with Lewy bodies, Parkinson's disease without dementia, multi-system arrophy and/or progressive supranuclear palsy, and for screening or arrophy and/or progressive supranuclear palsy, and for screening or treat Alzheimer's disease and the other neurological diseases. The method is effective in the differential diagnosis of Alzheimer's disease versus corebrospinal fluid (CSP)-beta-amyloid synthetic peptide which is used in the exemplification of the present invention
                                                                                                                                                                                                                                         Cerebrospinal fluid; CSF; beta amyloid; differential diagnosis; neurological disease; Alzheimer's disease; neuroprotective; nootropic; dementic; Parkinson's disease; dementia; multi-system atrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for the differential diagnosis of an individual suffering from Alzheimer's disease versus an individual suffering from another neurological disease involves use of phospho-tau as a neurological
                                                                                                                                                                                                        Cerebrospinal fluid (CSF)-beta-amyloid synthetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "phosphorylated threonine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vanmechelen E, Vanderstichele H, Hulstaert F;
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "acetylated"
                                                                                             ABB05625 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 18; 37pp; English.
                                                                                                                                                                                                                                                                                                    progressive supranuclear palsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2001; 2001WO-EP007029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000EP-00870151.
18-JUL-2000; 2000US-0218907P.
                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INNO-) INNOGENETICS NV.
----- PSSGE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-171654/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200203073-A1
                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                     23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                  ABB05625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marker.
                                                                                                                                                                                                                                                                                                                                          Homo
                                                                           ABB05625
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Local Similarity 29.6 nes 21; Conservative

Matches

236 LPLPTTPSSGE 246

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                generating a mammalian immune response directed to the protein of Pi; (5) detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related protein or a 254PlD6B-related polynuclectide; (6) a composition that modulates the status of a cell that expresses a protein of Pi; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9)
                                                                                                              176 PRGSAEYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New 254PID6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PID6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                                    1 PRGAAP-----PGOKGOANAT----RIPAKT------PPAPKTP---- 29
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254PID6B; small interfering RNA; siRNA; immune response;
254PID6B-related protein; cytostatic; gene therapy; cancer; human;
                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
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                                    Length 34;
                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Challita-Eid PM,
                                    Score 61.5; DB 5;
Pred. No. 3.2e+03;
                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; SEQ ID NO 41; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jakobovits A,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human 254P1D6B peptide SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                              ADR00630 standard; peptide; 12 AA.
                                      1.18;
29.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-2004; 2004WO-US001965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JAN-2003; 2003US-0442526P
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kanner SB, Raitano AB, J
Perez-Villar JJ, Faris M;
                      Query Match
Best Local Similarity 29.6%
                                                                                                                                                                                          236 LPLPTTPSSGE 246
                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                -----PSSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-580991/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004067716-A2.
Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                    ADR00630;
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             hybridoma that produces the antibody; (11) delivering a cytotoxic agent to a delighestic agent to a cell that expresses the protein of Pi; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of Pi. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254PID6B; small interfering RNA; siRNA; immune response;
254PID6B-related protein; cytostatic; gene therapy; cancer; human;
a non-human transgenic animal that produces the antibody; (10) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
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                                                                                                                                                                                                           ; DB 8; Leng...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Challita-Eid PM,
                                                                                                                                                                                                                       Score 60; DB & Pred. No. 7.8e+0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; SEQ ID NO 137; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jakobovits A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 254P1D6B peptide SEQ ID NO:137.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR00726 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-2004; 2004WO-US001965.
                                                                                                                                                                                                                         1.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-2004 (first entry)
                                                                                                                                                                                                                       Query Match 1.1
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                       151 EEMSEYXDDYRE 162
                                                                                                                                                                                                                                                                                                                            1 EEMSEYSDDYRE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perez-Villar JJ, Faris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-580991/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004067716-A2.
                                                                                                                                                                                        Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR00726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kanner
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                       ADR00726
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hybridoma that produces the antibody; (11) delivering a cyctoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cycostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                        detecting, in assimple, the presence of a 254PlD6B-related protein or a 254PlD6B-related polynucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a
generating a mammalian immune response directed to the protein of Pl; (5)
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Sequence 9 AA;

Gaps ö 0; Indels 1.1%; Score 59; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0; Indels Ouery Match
Best Local Similarity 100...
Best Acad 9; Conservative 929 RCICSHLWM 937 1 RCICSHLWM 9 ò 셤

RESULT 15 ADR00838

ADR00838 standard; peptide; 9 AA. (first entry) 04-NOV-2004 ADR00838; 

Human 254P1D6B peptide SEQ ID NO:249.

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human;

chromosome 6.

Homo sapiens,

WO2004067716-A2

12-AUG-2004.

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P

(AGEN-) AGENSYS INC

Ge ₩; Jakobovits A, Challita-Eid PM, Perez-Villar JJ, Faris M; Kanner SB, Raitano AB,

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 9; SEQ ID NO 249; 345pp; English.

ö The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PlD6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous coursected sin length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (PI, see SEQ ID

any of the 42 lists of peptides, given in the specification, or a protein any of the 42 lists of peptides, given in the specification, or a protein that is at least 80, 91, 92, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that the at lull complement of the polynucleotide described above; (4) a generating a mammalian immune response directed to the protein of P1; (5) generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254P1D6B-related polynucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human composition that comprises the composition described above in a human annohuman transgenic animal that produces the antibody; (10) a phoridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and composition or survival of cancer cells that express the protein of P1. 254P1D6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254P1D6B gene is located on chromosome 6p22. \$

Sequence 9 AA;

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. 0 0; Indels Length 9; 1.1%; Score 59; DB 8; Le 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; 

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Gaps

ò 셤 Search completed: October 12, 2005, 10:29:17 Job time : 75 secs

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254PlD6B-related polynuclectide; (6) a composition that modulates the status of a cell that expresses a protein of Pl; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cycloxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of Pl. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B v.5, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22. 88888888888888888

Sequence 1072 AA;

ô Gaps ö Score 5576; DB 8; Length 1072; Pred. No. 0; 0; Mismatches 3; Indels 0; 99.9%; Best Local Similarity 99.7 Matches 1069; Conservative Query Match

MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTPPVVDCTAA Н

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9 9 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA

120 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 61

LINRGSPSGIWGDSPEDIRKDLTFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSA 180 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA 61 121

EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT 121 181

240 181

TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST TPSSGEVLEKEKASQLOEOSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST 241

300

300 360 360

EHSI PTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP 301 301

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NUTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE 421 421

481 481 LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK 541 601

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EHVRGPSAVEMENI DKAI ATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR 199 661 721 840

781 LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGVGQLTEQRKDTLVRQ

RESULT 3

ADRIGO ADRIgora ADRIgor 540 780 099 099 720 780 480 480 900 900 KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTPQLK VTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW VTDSSRQQSTAVVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW EHVRGPSAVEMENI DKALATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN **ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN** 541 721 601

1020 1020 960 840 900 960 LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLMMENLIQRYIWDGESNCEWSIFYVT VLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 961 VLAFTLIVLTGGFTWLCICCCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ LAVILINVLDSDIKVOKIRAHSDLSTVIVFYVOSRPPFKVLKAABVARNI,HMRLSKEKADF LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1021 841 901 901 961 a a 셤 성 암 셤 ò 8 8

Ź ADR00601 standard; protein; 1072 04-NOV-2004 (first entry) ADR00601;

Human 254PlD6B v.6 protein SEQ ID NO:12.

254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.6; chromosome 6.

WO2004067716-A2 Homo sapiens.

23-JAN-2004; 2004WO-US001965

12-AUG-2004.

24-JAN-2003; 2003US-0442526P.

(AGEN-) AGENSYS INC.

3 ge Challita-Eid PM, Kanner SB, Raitano AB, Jakobovits A, Perez-Villar JJ, Faris M;

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 1; SEQ ID NO 12; 345pp; English.

The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the case 254P1D6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous conclectides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID NO:3, 5 or 7 ABN00592, ABR00594 or ABR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein chat is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5)

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detecting, in a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the catatus of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P1D6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254P1D6B v.6, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on chromosome 6p22.
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99.9%; Score 5574; E
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 541 Н 421 61 61 121 121 181 181 241 241 301 361 361 421 481 481 541 601 601 661 721 301 요 g ò g ઠે 셤 ò 셤 유 à g ò 셤 ò 셤 ò g Š ద ò 요 Š 8

VLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020 The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PlD6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl. see SEQ ID NO.3; 5 or 7 ADRO0592, ADRO0599, or a peptide included inniny of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entries amino acid sequence of Pl; (2) a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide that is a full complement of the polymucleotide described above; (4) 960 840 960 New 254PID6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PID6B protein or corresponds to a subsequence of the ORF, useful for detecting LVEGVYTFHLRVIDSQGASDIDTATVEVQPDPRKSGLVELILQVGVGQLIEQRKDTLVRQ LAVLLINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT LIFEKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 961 VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ LAVLLINVLDSD1KVQK1RAHSDLSTV1VFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF 1072 254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.1 clone LCP-3; chromosome 6. EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 3 g PM, Challita-Eid Human 254P1D6B v.1 clone LCP-3 protein SEQ ID NO:8. Example 1; SEQ ID NO 8; 345pp; English. Jakobovits A, M; Ā ADR00597 standard; protein; 1072 23-JAN-2004; 2004WO-US001965 24-JAN-2003; 2003US-0442526P (first entry) Kanner SB, Raitano AB, Perez-Villar JJ, Faris treating cancer. (AGEN-) AGENSYS INC. WPI; 2004-580991/56. WO2004067716-A2 Homo sapiens. 04-NOV-2004 12-AUG-2004. 1021 ADR00597; 1021 901 901 196 781 841 781 841 and ADRO0597

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generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PloBe-related protein or a 254PloBe-related polyucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cyctoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B v.1 clone LCP-3, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome
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                                                                                               LVEGVYTFHLKVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ
                                                                                                                                                                                                              VLAFTLIVLTGGFTWLCICCCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST
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ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN
                                                            LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ
                                                                                                                                                                                                                                                                                                    LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; 254PID6B v.2; chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 9; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human 254PlD6B v.2 protein SEQ ID NO:9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Perez-Villar JJ, Faris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and treating cancer.
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that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PlbGB-related protein or a 254PlbGB-related protein or a 254PlbGB-related protein or a capture of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition that modulates the composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a disposition and produces the antibody; (11) delivering a cytotoxic agent car a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproducin or survival of cancer cells that express the protein of P1. 254PlbGB has cytostatic activity, and can be useful for treating and detecting cancer. The present sequence represents the human 254PlbGB y.2, which is used in the exemplification of the present invention. The human 254PlbGB gene is located on chromosome 6p22. 

Sequence 1072 AA;

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ö 180 120 240 9 99 9 720 720 120 180 240 300 300 360 420 480 480 540 540 900 EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP 360 APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV 420 9 VIDSSRQQSTAVVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW KTSVDSPVLRISNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK VTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKEL1FPVESATLDGSSSSDDHGIVFYHW EHVRGPSAVEMENI DKA I ATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR 181 EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYINESASTPAPKLPERSVILPLPT NVTVKPARRVNLPPVAVVSPQLQELTLELTSALIDGSQSTDDTEIVSYHWEEINGPFIEE 1 MAPPITGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA 61 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 121 LNRGSPSGIWGDSPEDIRKDLPFLGKDWGLEEMSEYADDYRELEKDLLQPSGKQEPRGSA 241 TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST EHSIPTPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP 361 APPUETTYNYEWNLISHPIDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK 1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGP1RSYLTFVLRPVQRPAQLLDYGDMM LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST NVTVKPARRVNI PPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE Gaps ; 0 Length 1072; Indels ij, 8; В Score 5574; DE Pred. No. 0; 0; Mismatches Query Match 99.9%; Best Local Similarity 99.7%; Matches 1069; Conservative ( 421 301 541 421 481 541 601 601 661 661 301 361 481 19 121 181 241 셤 ద 유 a a ð ઠે

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VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020 960 780 840 840 900 900 LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 960 New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting 961 VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTLLDNMDEQERMELRPKYGIKHRST LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ LAVILINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF LAVLIAVIDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF 254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.1; chromosome 6. EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 3 g Challita-Eid PM, Human 254P1D6B v.1 amino acid sequence SEQ ID NO:259. Example 13; SEQ ID NO 259; 345pp; English. Jakobovits A, M; ADR00848 standard; protein; 1072 AA 23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P. (first entry) Kanner SB, Raitano AB, Perez-Villar JJ, Faris WPI; 2004-580991/56. (AGEN-) AGENSYS INC. and treating cancer. WO2004067716-A2 Homo sapiens. 04-NOV-2004 12-AUG-2004. 841 ADR00848; 721 781 901 901 961 1021 1021 841 781 RESULT 6 ADR00848 용 셤 염 g à 임 ઠે ò ð ઠે

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to 254PID6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous mucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID NO.3, sor 7 ARROSS22, ARROSS24, or ABROSS96), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or

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identical to an entire amino acid sequence of P1; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related protein or a 254PlD6B-related protein or a cast that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human cunit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cyctoxic agent or a diagnostic agent to a cell that expresses the protein of P1, 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful cor treating and detecting cancer. The present sequence represents a human 254PlD6B vi amino acid sequence, which is used in the composition of the present invention. The human 254PlD6B gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       located on chromosome 6p22
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Sequence 1072 AA;

540 900 300 180 240 300 360 360 420 420 480 480 540 900 99 99 720 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 120 LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA 180 9 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA LINRGSPSGIWGDSPEDIRKDLPFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSA TPSSGEVLEKEKASOLOEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALI VNNAVDYPPVANAGPNHTIT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK VIDSSRQOSTAVVIVIVOPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW HUNGPSAVEMENIDKAIATVTGLQVGTYHPRLTVKDQQGLSSTSTLTVAVKKENNSPPR MAPPTGVLSSLLLLVTIAGCARKOCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT TPSSGEVLEKEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV 361 APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK VTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKEL1FPVESATLDGSSSSDDHGIVFYHW EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR Gaps ö 99.9%; Score 5574; DB 8; Length 1072; 99.7%; Pred. No. 0; ive 0; Mismatches 3; Indels 0; Best Local Similarity .... Matches 1069; Conservative 541 -181 61 241 301 121 121 181 241 421 601 601 561 Query Match 61 301 361 421 481 481 541 셤 g ઠે ద ઠે a Š 음 장 g 8 8 8 a ò 셤 ð g ò ઠે

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That is at least 90, 91, 93, 94, 95, 96, 97, 98, or 94% homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 94% homologous or identical to an entire amino acid sequence of P1; (2) a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide that is a full complement of the polymucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related protein or P1; (7) a pharmaceutical composition that compresses a protein of P1; (7) a pharmaceutical composition that compresses a protein of P1; (7) a pharmaceutical composition that composition described above in a human composition that produces the entibody or its fragment, which is monoclonal; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cyclotoxic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cycostatic activity, and can be capted in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B y.2, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22. peptide included in 5 or 7 ADR00592, ADR00594 or ADR00596), 

Sequence 1072 AA;

Gaps 0; Length 1072; Indels 3, ., B 0; Mismatches Score 5574; Pred. No. 0; 99.94; Best Local Similary, Matches 1069; Conservative Query Match Best Local Similarity

1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA

RESULT

9 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA

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VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020 720 780 780 840 900 900 960 LVEGVYTFHLRVTDSQGASDTDTATVEVQPPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ LAVLLINVLDSD1KVQK1RAHSDLSTV1VFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMBLRPKYGIKHRST LVEGVYTPHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 901 961 1021 1021 721 781 901 961 841 841 199 721 781 a 셤 8 셤 Š 요 ò g ò 임 ò δ

254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.1 clone LCP-3; chromosome 6. Human 254PlD6B v.1 clone LCP-3 protein SEQ ID NO:3. ADR00592 standard; protein; 1072 AA (first entry) 04-NOV-2004 ADR00592;

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WO2004067716-A2 12-AUG-2004. 24-JAN-2003; 2003US-0442526P. (AGEN-) AGENSYS INC.

23-JAN-2004; 2004WO-US001965.

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9 9 Challita-Eid PM, Jakobovits A, M; Kanner SB, Raitano AB, Perez-Villar JJ, Faris

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2004-580991/56. N-PSDB; ADR00591 New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B

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or corresponds to a subsequence of the ORF, useful for detecting

Claim 1; SEQ ID NO 3; 345pp; English.

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254P1D6B protein, or corresponds to a subsequence of the oncodes the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous contiguous aniho acids of a protein of figure 2 (Pl. see SEQ ID nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous aniho acids of a protein of figure 2 (Pl. see SEQ ID NO:3), 5 or 7 ADRO0559, or appetide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) confecting, in a sample, the presence of a 254P1D6B-related protein or a conference of a 254P1D6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; (3) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P1D6B has cytostatic activity, and can be composition in gene blrapy. The composition or survival of cancer cells that express the human 254P1D6B victone is need in the exemplification of conference of the present invention. The human 254P1D6B gene is located on chromosome conference or the present invention. The human 254P1D6B gene is located on chromosome conference.

Sequence 1072 AA;

ô 1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA Gaps ö DB 8; Length 1072; Indels .; 99.9%; Score 5574; I 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 1072; Conservative Query Match ઠ

CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 120 9 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 61 19 셤 \$ 요

121 LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA 180 LINRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSBYXDDYRELEKDLLQPSGKQEPRGSA **EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT** 121 181

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**EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT** TPSSGEVLEKEKASQIQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST 241 TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST 181 241

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EHSI PTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLI TLPDNEVELKAFVAP EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP 301 301

APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGPV

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361 APPVETTYNYEWNLISHPIDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV 421 NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE 421

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ADR00862 standard; protein; 1053 AA. 04-NOV-2004 (first entry) ADR00862; 

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Human 254PlD6B v.1 protein sequence SEQ ID NO:273.

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.1; chromosome 6.

Homo sapiens

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240 300 300 360 360 420 420

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WO2004067716-A2

12-AUG-2004.

23-JAN-2004; 2004WO-US001965

24-JAN-2003; 2003US-0442526P

(AGEN-) AGENSYS INC.

3 9 Ψ, Challita-Eid Kanner SB, Raitano AB, Jakobovits A, Perez-Villar JJ, Faris M;

WPI; 2004-580991/56.

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New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                         and treating cancer.
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Example 5; SEQ ID NO 273; 345pp; English.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to composition that comprises a double stranded siRNA that corresponds to composition that comprises the nucleotides in length. Also described: 1, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 [P1, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00569, or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein cot that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5) a generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PID6B-related protein or a composition that modulates the composition that comprises the composition described above; (1) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that expresses the protein of P1; (1) a non-human transgenic animal that expresses the protein of P1; (1) a non-human transgenic animal that expresses the protein of P1; (1) a non-human transgenic animal that expresses the protein of P1; (1) a non-human transgenic animal that expresses the protein of P1; (1) a non-human transgenic animal that expresses the protein of P1; (1) a non-human transgenic animal that express the protein of P1; (2) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PID6B has cytostatic activity, and can be human 254PID6B v1 protein sequence, which is used in the expression of the present invention. The human 254PID6B gene is located or survival of successing th

Sequence 1053 AA;

Gaps ö 8; Length 1053; Indels 3; 8 Score 5485; DB Pred. No. 0; 0; Mismatches 98.3%; Best Local Similarity 99.7 Matches 1050; Conservative Query Match

120 VSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK 139 79 9 CARKOCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWFEGRCYL CARKQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL VSCPHKENCEPKKMGPIRSYLIFVIRPVQRPAQLLDYGDMALNRGSPSGIWGDSPEDIRK 20 80 61 셤 셤 ઠ ઠે

DLPFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV 180 DLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV 121 140

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259 240 319 300 379

GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ 200 181 260

SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS ELPI SPTTAPRITVKELIVSAGDNLI I TLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT 241 320 301

PQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNY 499 DY OGE I KOCHKOTLILISQLSVGLYV FKVTVSSENA FGEGFVNVTVKPARRVNLPPVAVVS 440 361

DYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVS

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961 CCKRQKRIKIRKKIKYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDT 1020 CCKROKRIKIRKKTKYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDT 1039 979 480 540 619 9 619 9 739 720 799 780 859 840 919 ENNRPPVAVAGEDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGFSAVEMENIDKAIA TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD DIDIATVEVOPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA 901 HGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCIC VLYEWSLGPGSEGKHYVVMQGVQTPYLHLSAMQEGDYTFQLKYTDSSRQQSTAVVTVIVQP ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS DIDIATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA HGHCDPLTKRCI CSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCIC SFRITVIDS DGATNSTTAALI VNNAVDY PPVANAG PNHTITL PONSITLNGNOSSDDHQI HSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSG VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQP IFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 1040 841 980 481 541 680 740 800 781 860 920 200 560 620 601 661 721 421 ઠ g q à 셤 ò a ò 셤 ઠે g 8 셤 ò 원 ઠ g ò ò

Æ ADR00863 standard; protein; 1053 04-NOV-2004 (first entry) 1021 ADR00863; RESULT 10 ADR00863

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254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.3; chromosome 6. Homo sapiens. 

Human 254P1D6B v.3 protein sequence SEQ ID NO:274.

23-JAN-2004; 2004WO-US001965. WO2004067716-A2 12-AUG-2004.

24-JAN-2003; 2003US-0442526P.

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e Challita-Eid PM, Jakobovits A, Kanner SB, Raitano AB, Ja Perez-Villar JJ, Faris M; (AGEN-) AGENSYS INC.

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the cate of the nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID ONC3, 5 or 7 ADR00929, ADR00596), or a peptide in included in any of the 42 lists of peptides of sequence of P1; (2) a polynucleotide that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous consists escenting of encourage of the encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) detecting in a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition that modulates the composition that comprises the composition does form; (8) an antibody or its fragment, which is monoclonal; (9) which does form; (8) an antibody or its fragment, which is monoclonal; (9) which does form; (9) an antibody or its fragment, which is monoclonal; (9) which does form; (9) an antibody or its fragment, which is monoclonal; (9) which does form; (9) and the protein or a composition that produces the antibody; (10) a pharmaceutical composition that produces the antibody; (10) a pharmaceutical composition animal that produces the antibody; (10) a pharmaceutical composition animal that produces the antibody; (10) a pharmaceutical composition animal that produces the antibody; (10) a pharmaceutical composition animal that produces the antibody; (10) a pharmaceutical composition animal that produces the antibody or its fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hybridoma that produces the antibody; (11) delivering a cytocoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P106B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254P106B v.3 protein sequence, which is used in the exemplification of the present invention. The human 254P106B gene is located on
                                                                       New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                       Example 5; SEQ ID NO 274; 345pp; English.
                                                                                                                                                                                   treating cancer.
2004-580991/56
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Sequence 1053 AA

ö 139 VSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK 120 180 259 240 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS 319 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS 300 379 360 DLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV 199 DYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVS 439 1 CARRQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL 60 DLPFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ ELPISPTTAPRTVKELTVSAGDNIIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT CARKQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL 80 VSCPHKENCEPKKOMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEXEKASQLQEQ ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT Gaps ö Length 1053; Indela 3; 8; 8 0; Mismatches Score 5485; Pred. No. 0; 98.3%; Conservative Similarity Matches 1050; 20 61 260 241 320 301 380 361 Query Match 140 121 200 181 Local 용 셤 δ 셤 δ 8 음 장 유 8 6 ⋧

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                                                                                                                                                         ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA
                                                                                                                                                                                                          DIDIAIVEVQPDPRKSGLVELILQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA
                                                                                                                                                                                                                                                                                                                                                        VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAVVTVIVQP
                                                                                                                                                                                                                                                         GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLINLVEGVYFFHLRVTDSQGAS
                                                                                                                                                                                                                                                                                                                                            HSDLSTVI VFYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSG
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             PQLQELTLPLTSALIDGSQSTDDTEIVSYHWEBINGPFIEEKTSVDSPVLRLSNLDPGNY
                                               SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI
                                                              SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPONSITLNGNOSSDDHOI
                                                                                            VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTPQLKVTDSSRQQSTAXVTVIVQP
                                                                                                                                             ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA
                                                                                                                                                                                             TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD
                                                                                                                                                                                                                                             GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS
                                                                                                                                                                                                                                                                                            DIDIATVEVQPDPRKSGLVELILQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA
POLOELTLPLTSALIDGSOSTDDTEIVSYHWEBINGPFIEBKTSVDSPVLRLSNLDPGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254P1D6B; small interfering RNA; siRNA; immune response;
254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
254P1D6B v.3; chromosome 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 254PlD6B v.3 protein sequence SEQ ID NO:272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1021 IFSREXMERGNPKVSMNGSIRNGASFSYCSKDR 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1040 IFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072
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The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous corresponds to a subsequence of the ORF, where the consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADRO0552, ADRO0594 or ADRO0556), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of Pl; (2) a polymuclectide that encodes the protein; (3) a composition comprising a polymuclectide that is a full complement of the polymuclectide described above; (4) composition in a sample, the presence of a 254PID6B-related protein or a composition that modulates the status of a cell that expresses a protein of Pl; (7) a pharmaceutical composition that comprises the composition described above in a human composition that comprises the composition of Pl; (10) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and con-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and con-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and con-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent, reproduction or survival of cancer cells that expresse the protein of Pl; 254PID6B has cytostatic activity, and can be human 254PID6B v.3 protein sequence, which is used in the exemplification.
                                                                                                               New 254PID6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PID6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                                                                                                                                                Example 5; SEQ ID NO 272; 345pp; English.
                                                         2004-580991/56.
Perez-Villar JJ,
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98.3%; Score 5485; DB 99.7%; Pred. No. 0; 0; Mismatches Similarity Sequence 1063 AA; Query Match

ö 71 VSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMALNRGSPSGIWGDSPEDIRK 130 199 259 319 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS 310 370 VSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK 139 131 DLPFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV 190 ELPISPITAPRIVKELIVSAGDNLIIILPDNEVELKAFVAPAPPVETIYNYEWNLISHPT 379 70 79 ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT GDSPAVPAETQODPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEO DLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS 20 CARKQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL Gaps ö 8; Length 1063; 3; Best Local Similaricy .... Matches 1050; Conservative 311 80 200 260 251 320 140 191 셤 g g 원 셤 ð 셤 ò δ ò ઠે

CCKROKRIKIRKKIKYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDT 1039 979 970 430 499 490 559 550 619 610 619 670 739 TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD 730 799 859 850 919 HSDLSTVIVFYVQSRPPFKVLKAAEVARNLHWRLSKEKADFLFKVLRVDTAGCLLKCSG HGHCDPLTKRCICSHLMMENLIQRYIWDGESNCEWSIRYVTVLAFTLIVLTGGFTWLCIC HGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCIC PQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNY VLYEWSLGPGSEGKHVVWQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAVVTVIVQP ENNR PPVAVAGPDKELI FPVESATLDGSSSSDDHGI VFYHWEHVRGPSAVEMENI DKAIA ENNR PPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS 491 SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLFQNSITLNGNQSSDDHQI VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQP TVTGLQVGTYHPRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD DIDIATVEVOPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA HSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSG SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI IFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 1040 1031 431 851 911 971 200 260 620 680 740 731 800 791 860 920 980 440 371 551 611 671 g 셤 셤 g à 엄 ò g ð 셤 ઠ 셤 ઠે 셤 ð 셤 ò 셤 δ ò ð ò

254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.3; chromosome 6. Human 254P1D6B v.3 protein SEQ ID NO:7. ADR00596 standard; protein; 1063 AA 23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P. (first entry) WO2004067716-A2. 04-NOV-2004 Homo sapiens 12-AUG-2004 TO NAME OF THE PARTY OF THE PAR

(AGEN-) AGENSYS INC.

380 DYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVS 439

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The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PID6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists as length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pt, see SEQ ID NO:3, 5 or 7 ADRO0592, ADRO0594 or ADRO0596), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98* homologous or that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) cannoplement of the presence of a 254PID6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition described above; (10) a non-human transgent animal that produces the antibody; (11) delivering a cytocoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and con-human transgenic animal that produces the antibody; (11) delivering a cytocoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and con-human iransgenic animal that produces the antibody; (11) delivering a cytocoxic agent or a diagnostic agent to a cell that expresses the protein of P1; 254PID6B has cytostatic activity, and can be captured by in gene therapy. The composition or survival of cancer cells the expresses the protein of P1; 254PID6B will be a captured on chromosome of the present in the exemplification of the present content of the present
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ive 0; Mismatches
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Best Local Similarity 99.7
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                     Kanner SB, Raitano AB,
Perez-Villar JJ, Faris
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             PQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNY
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254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
254P1D6B v.3; chromosome 6.
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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the nucleotides protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous mucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl. see SEQ ID NO.3, 5 or 7 ADRO0592, ADRO0594 or ADRO0566), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein composition that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 994 homologous or identical to an entire amino acid sequence of Pl: (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) composition that is a sample, the presence of a 254PIDGB-related polymucleotide; (6) a composition that modulates the composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the protein of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B v. 3, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                       New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
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                                                                                            PM,
                                                                                            Challita-Eid
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 10; 345pp; English.
                                                                                            Jakobovits A,
                                                                                                                             Faris M;
                                                                                            Raitano AB,
                                                                                                                                                                                         2004-580991/56.
                                 (AGEN-) AGENSYS INC
                                                                                                                          Perez-Villar JJ,
                                                                                            SB,
                                                                                            Kanner
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Score 5485; DB 8; Length 1063; Pred. No. 0; 0; Mismatches 3; Indels 0; 98.3%; Matches 1050; Conservative Local Similarity Sequence 1063 AA; Query Match

ö 130 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS 310 259 250 ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT 379 80 VSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK 139 DLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV 199 DLPFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV 190 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTTPPTSAAPSESTPS 319 79 70 VSCPHKENCEPKKAGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK CARKQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ Gaps ö 131 320 20 11 140 200 191 260 251 셤 원 유 ò ò 셤 셤 ò 8 à ò

1030 CCKROKRIKIRKKTKYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDT 1039 430 499 490 559 550 619 610 619 670 739 730 799 790 859 919 910 979 911 HGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLFGGFTWLCIC 970 ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT SFRLIVIDSDGAINSTIAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQP ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS DTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA HGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCIC DYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVS POLOELTLPLTSALIDGSOSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNY SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI VI.YEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAVVTVIVQP GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS DIDIATVEVOPDPRKSGLVELTLOVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA HSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSG 1040 IFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 560 851 1031 791 860 440 680 740 800 920 980 971 551 620 311 380 200 191 511 671 731

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ADG14994 standard; protein; 978 (first entry) Human SECP-27 protein. 26-FEB-2004 ADG14994; RESULT 14 ADG14994

antidiabetic; cytostatic; dermatological; immunosuppressive; antidiabetic; cytostatic; dermatological; immunosuppressive; darmatological; immunosuppressive; darmatinitalmanatory; thyrominetic; antiallergic; cerebroprotective; gastrointestinal; hepatotropic; nephrotropic; anticonvulsant; antibacterial; antiparasitic; fungicide; protozoacide; viroide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HV; notropic; neurodegenerative; Parkinson's disease; Alzheimer's; muscular; myotonic dystrophy; catatonia; endocrine; diabetes; Grave's; leukaemia; cervical; breast cancer; immunological; scleroderma; gastrointestinal; Crohn's; renal; Goodpasture's syndrome; viral infection; bacterial; fungal; parasitic; protozoal; helminthic; cardiovascular; atherosclerosis; hepatic; TAMES AND A STAN

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                                                                                                                                                                                            LVEGVYTFHIRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ
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                                                                                                                  TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST
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                                     TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST
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                EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT
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Complypeptide. The polypeptide of the invention demonstrates

Comeroprocective, relaxant, antithyrood, antidiabetic, cytostatic,

dermatological, immunosuppressive, antiinflammatory, thyromimetic,

antiallergic, cerebroprotective, gastrointestinal, hepatotropic,

compliant antiparsitic, antiparkinsonian, antibacterial,

antiparsasitic, fungicide, protozoadide, viucide, uropathic,

antirheumatic, cardiant, cardiovascular, anti-HIV and nootropic,

antirheumatic, cardiant, cardiovascular, anti-HIV and nootropic

continities. The polypeptide may be useful in diagnoshing, preventing and

treating disorders including neurodegenerative disorders such as

Composition dystrophy and catatonia, endocrine disorders particularly

chabetes and Grave's disease, cancers such as leukaemia, cervical or

breast cancer, immunological disorders including scleroderma, systemic

charbetes and Grave's disease, cancers such as leukaemia, cervical

charbetes and disease, renal disorders engencers

composition's disease, renal disorders engencers

comparaticularly Crohn's disease, renal disorders engencers

comparation's disease, renal disorders engencers

comparation's disease, renal disorders engencers

comparation's diseases, renal disorders engencers

comparation's diseases particularly viral, bacterial, fungal, parasitic,

protozoal, helminthic, cardiovascular disorders engencers

cond hepatic diseases particularly cirrhosis. The polynucleotides may be

consent therapy procedures. The current sequence is that of the human SECP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer
                                                                                                                                                                                                                                                                                                                                     Marquis JP, Lee SY, Elliott VS, Ramkumar J, Hafalia AJA;
Kable AB, Chawla NK, Emerling BM, Khare R, Jiang X, Jackson AA;
Hawkins PR, Jin P, Mason PM, Richardson TW, Swarnakar A, Lal PG;
Warren BA, Lee S, Griffin JA, Fu GK, Wilson AD, Xu Y, Bulloch S,
Becha SD, Bhatia UG, Burrill JD, Blake JJ, Ho A, Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0;
1; Mismatches
gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 27; 300pp; English.
                                                                                                                                                                                            05-APR-2002; 2002US-0370707P.
19-APR-2002; 2002US-0373824P.
03-MAY-2002; 2002US-0377883P.
24-MAY-2002; 2002US-0383218P.
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99.6%;
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  cirrhosis; transgenic;
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nes 949; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. neuromuscular, and/or infections.
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                                                                          WO2003087300-A2.
                                                                                                                                                       01-APR-2003;
                                       Homo sapiens
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This invention relates to novel membrane proteins that are associated with differentiation and/ or metabolic function of adipocytes, in particular of mouse origin. Specifically, it refers to the isolated nucleic acid molecules encoding all or part of these proteins, appropriate antibodies and screening assays useful for the development of drug compositions derived thereof. The present invention describes these compositions as useful for the treatment of diseases associated with abnormalities of adipocyte function, such that they can be used to prevent, treat or diagnose obesity, hypertension, hyperlipaemia, diabetes and arteriosclerosis. Accordingly, they exhibit anorectic, antidiabetic, antiarteriosclerotic, antilipaemic and hypotensive activities. This polypeptide is a murine membrane protein sequence related to adipocyte function of the invention.
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                                     09-JUL-2003; 2003WO-JP008690
                                                                                                         10-JUL-2002; 2002JP-00201856.
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N-PSDB; ADM36226.
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Search completed: October 12, 2005, 10:02:48 Job time : 131 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein

October 12, 2005, 10:00:24 Run on:

; Search time 128 Seconds (without alignments) 4288.663 Million cell updates/sec

US-10-764-390-3 Title: Perfect score:

1 MAPPIGVLSSLLLLVTIAGC......vSMNGSIRNGASFSYCSKDR 1072 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues

Searched:

Total number of hits satisfying chosen parameters:

1612378

length: 0 length: 2000000000 seq 88 Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9y4g7 homo sapien	mus r	Q718r6 homo sapien	mus n	Q8bhu7 mus musculu	Q8bhz3 mus musculu	Q6pjj7 homo sapien	homo	homo	homo	homo	homo	mus m		-		anop	homo	homo	рошо	Q7ytz3 drosophila	homod	homo	symb:	Q89pb9 bradyrhizob		rhodo	homo	homo	homo	O8tse7 methanosarc
SUMMARIES	Q1	Q9Y4G7	Q80U39	Q7L8R6	Q8K135	Q8BHU7	Q8BHZ3	Q6PJJ7	Q8IZA0	Q8WYZ5	QBNDAO	Q9H7V0	096770	Q8VBZ9	QBBHRS	63SA6Ö	09н9г2	0708G8	Q8N2B3	Q8WY39	Q961C3	Q7YTZ3	095010	Q9BUW6	Q67RJ0	Q89PB9	Q8E9W3	Q7UY44	Q8WZB3	Q8WZ42	Q10466	Q8TSE7
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## ALIGNMENTS

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MEDLINE=97349984; PubMed=9205841;
MEDLINE=97349984; PubMed=9205841;
Nagase T., Ishikwa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Tanaka A., Kotani H., Nomura N., Ohara O.;
Tanaka A., Kotani H., Nomura N., Ohara O.;
Tanaka A., Kotani H., Nomura N., Ohara O.;
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res 4.141-150(1997).
Genew, HGNC:21580; KIAA0319.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                PRT; 1109 AA
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Interpro; IPR000601; PKD.
SMART; SM00060; FN3; 4.
SMART; SM00089; PKD; 5.
                                                                                                Q9Y4G7; Q9UJC8;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                        KIAA0319 protein (Fragment)
Name=KIAA0319;
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SEQUENCE 1109 AA; 1219
                                                                    PRELIMINARY;
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SEQUENCE FROM N.A.
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                                        EHSIPTPPTSAAPSESTPSELPISPTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP
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TPSSGEVLEKEKARASQLOEQSSNSSGKEVIAPSHSLPPASLELSSVTVEKSPVLTVTPGST
                                                                   APPVETTYNYEWNL1SHPTDYQGE1KQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV
                                                                               NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE
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                                                                                                                                             KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT
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O1-JUN-2003 (TrEMBLrel. 24, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 26, Last annotation update)
MKIAA0319 protein (Fragment).
MKIAA0319 protein (Fragment).
Musme-D130043K2ZRik; Synonyms=mKIAA0319;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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TISSUE=Brain;
MEDLINE=22579291; PubMed=12693553;
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Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,

Nakajima D., Nagase T., Ohara O., Koga H.;

"Prediction of the coding sequences of mouse homologues of KIAA gene:
"I. The complete nucleotide sequences of 400 mouse KIAA-homologous
"Tandomly sampled from size-fractionated libraries.";

DNA Res. 10:35-48(2003).

REMBL; AKI22246; BAC65288.1;

REMBL; AKI22246; BAC65288.1;

RITEPPO; IPRO03691; FN III.

RITEPPO; IPRO06601; FN III.

RART; SM00060; FN3; 4.

SMART; SM00089; PKD; 5.

REMBL; PROSITE; PSS003; PKD; 2.

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SEQUENCE 1083 AA; 118201 MW; 788BBFEB3A7C02CE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCDLITCDLAWWFEGSCYLVKCMRSENCEPRITGPIRSYLTFVRRPVQRPGQLLDYGDWM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEINGPFIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPV
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                                                                                                                                                                                                                                                                                                                                                                    Score 4255.5; DB 2;
Pred. No. 2.5e-200;
1; Mismatches 160;
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75.8%;
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CETRAINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Altschul S.E., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.E., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

A Dokins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

A Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Hahey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Racinguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T Generation and initial analysis of more than 15,000 full-length human
                           241 RQQSTAVVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRG
                                                                                                                                      301 PSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601 LIVLIGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRSTEHNSS
                                                                                                                                                                                                                                                                                                                                                       421 YTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIVLTGGFTWLCICCCKROKRTKIRKKTXYTILDNMDEQERMELRPKYGIKHRSTEHNSS
                                                                                                                                                                                                              RHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGV
                                                                                                                                                                                                                                             RHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGV
                                                                                                                                                                                                                                                                                                                      YTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                          NVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKV
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RQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRG
                                                                                                       PSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rođentia, Sciurognathi, Muridae, Murinae; Mus.
NCBI_TaxID=10090;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
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SEQUENCE FROM N.A
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                         SPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNS
                                                                                                    EQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLH
                                                                                                                                                                                                              891 MRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGES
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DHSVALQLTNLVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
SMBL; AL031230; CAA20249.1; -.
GO; GO:0005020; Crambrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007156; P:homophilic cell adhesion; IEA.
InterPro; IPR0006126; Cadherin.
InterPro; IPR000601; PKD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    707 AA; 78402 MW; FC7D2A98D778DF46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amotation update)
DJ73M3.3 (KIAA0319 gene product) (Fragment).
Home acid73M23.3;
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Pred. No. 6.4e-172;
0; Mismatches 1;
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Best Local Similarity 99.9
Matches 706; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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Q7L8R6;
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DGESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQER 1006
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SEQUENCE FROM N.A.
STRAINE-2059L6.07 IISSUE=Heart;
MEDLINE-2079174; PubMed=1102159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Komoo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
 920 DGDSNCEWSVLYVIIASFVIVVALGILSWTTICCCKRQK-GKPKRKSRYKILDATD-QES
                                                  RNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS'BL/67; TISSUE=Heart; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hajashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRSUB=Heart;
STRAIN=CSPIB-16J; TISSUB=Heart;
The FANTOM CONSOLTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-673 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUB-Heart; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsuumoto H., Sakaguchi S., Ikagami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330027H07 product:HYPOTHETICAL 103.9 kba PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosto
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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                                                                                                                                                                                           Match 43.5%; Score 2426.5; DB 2; Length Local Similarity 48.1%; Pred. No. 1.1e-110; Les 519; Conservative 136; Mismatches 314; Indels
                  to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                F4D51DD6DE4C889D CRC64;
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Strausberg R.;
Submitted (MAY-2002) to the EMBL/Ge EMBL, BC028869; AAH28869.1; -. MGD; MGI:2140475; AU040320.
InterPro; IPR0003961; FN III.
InterPro; IPR0008957; FN III-like.
InterPro; IPR000601; PNJ.
SMART; SM00060; FN3; 4.
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STRAIN=CS7BL/6J; TISSUE=Cerebellum;
The FANTOM CONSORTIUM,
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SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Cerebellum;
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SEQUENCE FROM N.A.
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                                                 SEQUENCE FROM N.A.

C STRAIN=C57BL/GJ; TISSUB=Heart;
A dachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Hangaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasuah T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Okasaki Y.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Soqabe Y., Tagami M.,
A Tagawa A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Charu A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
EMBL; AKO84668; BAC39244.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 YPPVANAGPNQVITLPQNSITLFGNQSTDDHGITSYEWSLSPSSKGKVVEMQGVRTPALQ
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                      109;
"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
43.1%; Score 2403.5; DB 2; Length
Best Local Similarity 48.3%; Pred. No. 1.6e-109;
Matches 514; Conservative 135; Mismatches 307; Indels
                                                                                                                                                                                                                                                                                                                      SMART; SM00060; FN3; 4.
SMART; SM00089; FN3; 4.
SMART; SM00089; PKD; 5.
Hypothetical protein.
SEQUENCE 1085 AA; 119329 MW; 7E61DB6001A275E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 KNVSIHPEPS-----EHSSPVSG-
                                                                                                                                                                                                                                                                                InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III-like.
InterPro; IPR000601; PKD.
                                                                                                                                                                                                                                                                  MGD; MGI:2140475; AU040320
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Best Local Similarity
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                                                                           SSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTST
                                                                                                                                                                                                                                                                                              767 IDGSDHSVALQLINLVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS'BL/66; TISSUE=Cerebellum; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Carninci P., Hayashizaki Y.; Hiqih-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730047D20 product:HYPOTHERICAL 103.9 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation of a full-length mouse cDNA collection.";
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
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406

439 526 646

706 619 992

826

977

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DGESNCEWSIFYVTVLAPTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMDEQER 1006
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibeh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                     LPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFK
                                                                                                                                                       VTVSSENAFGEGFVNVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIV
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Polycystic kidney disease 1-like, isoform a.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Sano H.,
Saitoh H., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; MGI:2140475, AU040320.
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...Lularne=zu499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 LWWLEGMCFQADCSKPQSCQPFRTDSSNSML------IIFQKSQTTDD
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                                                                                                                                                                                                                    STRAIN=C57BL/G1 TISSUB=Cerebellum;
MEDLINE=C57BL/G1 TISSUB=Cerebellum;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=C57BL/G1 N. Aizawa K., Hazama T., Rashiro H., Itoh M., Sumi N., Ishil Y., Nakamura S., Hazama M., Nishiro T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yohazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; REKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 43.1%; Score 2403.5; DB 2; Length 1085; al Similarity 48.3%; Pred. No. 1.6e-109; 514; Conservative 135; Mismatches 307; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 XXVSIHPEPS-----EHSSPVSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1085 AA; 119437 MW; 64CCADE9B26E84E0 CRC64;
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SMART; SM00089; PKD; 5.
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                                                                                                                                                                  TLDGSKSSDDQKIISYLWEKTQGPDGVQLENANSSVATVTGLQVGTYVFTLTVKDERNLQ
                                                                                                                                                                                                                                                                                       823 QVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKA
                                                                                                                                                                                                                                                                                                                                                                                                                997 DINVSQLTERLKGMPIRQIGVLLGVLDSDIIVQKIQPYTEQSTKNVFFVQNEPPHQIFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   883 AEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            943 RYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1003 EQERMELRP--KYGIKHRSTEHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIR
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            TLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLS
                                                                                                                                  STSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPA
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01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
POLYCYSTIC kidney disease 1-related protein.
Polycystic kidney disease 1-related protein.
Eukano sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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SMART; SM00089; PKD; 5.
PROSITE; PS50093; PKD; 1.
SEQUENCE 1049 AA; 115717 MW; 1781BFCA3C765DEB CRC64;
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY163234; AAN61054.1; -.
InterPro; IPR00361; FN III.
InterPro; IPR000601; PKD.
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48.0%; Pred. No. 2e-109;
tive 134; Mismatches 313;
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Best Local Similarity
Matches 519; Conserv
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SEQUENCE FROM N.A.
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan R.J., Malek J.B., Gunaratra P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELS-----SVTVEKSPVLTVTPGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 43.0%; Score 2402; DB 2; Length 10
Best Local Similarity 48.0%; Pred. No. 1.8e-109;
Matches 519; Conservative 134; Mismatches 313; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;50093; PKD; 1.
1049 AA; 115584 MW; 5BDE6057CC09A649 CRC64;
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Submitted (SEP-2001) to the
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InterPro; IPR000601; PKD.
SMART; SM00089; PKD; 5.
PROSITE; PS50093; PKD; 1.
SEQUENCE 1049 AA; 115584
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                                                                                                                                                                                                                                                                                                                                                                             cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDVIDGSDHSVALQLINLVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQ 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAA 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVARNIHMRISKEKADFILFKVIRVDTAGCILKCSGHGHCDPLTKRCICSHLWMENLIQR 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSS
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                                                                                                                                                                                                                                                                           SECAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPER----SVLLPLPTTPSSGE
                                                                                                                                                                                                                                                                                                                                                                                                                  344 IITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTP
                                                                                                                                                                                                                                           Gaps
          Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                        95;
                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

OIN W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Zhac Qin W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Zhac Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF289597; AAL55781.1; -. SWART; SM00069; FN3; 4.

SWART; SM00069; FN3; 5.

PROSITE; PS50093; FKD; 1.

PROSITE; PS50093; FKD; 1.

PHYPOThetical procein.

SEQUENCE 946 AA; 103879 MW; B52C7F0BD0A60620 CRC64;
                                                                                                                                                                                  2; Length
                                                                                                                                                                                                        Indels
                                                                                                                                                                                 41.5%; Score 2316.5; DB 2;
llarity 50.9%; Pred. No. 2.5e-105;
Conservative 119; Mismatches 258;
        Chordata; (Primates; (
          Eukaryota; Metazoa;
Mammalia; Butheria;
MCBI_TaxID=9606;
sapiens (Human)
                                                                                                                                                                                              Similarity
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Best Local Simi
Matches 489;
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                                                                                                                                                                                  497 KAVDYPPVANAGPNQVITLPQNSITLFGNQSTDDHGITSYEWSLSPSKGKVVEMQGVRT
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                     ----SLIRKLOKRGSPSDVVTPIVTOHS--
                                             EVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELS----SVTVEKSPVLTVTPGS
                                                          -----PTSAAPSESTPSELPISPTTAPRTVKELTVSAGDN
                                                                                                        LITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGL
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Last sequence update)
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                        -----RPAVSSSDQQ-
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Q8WYZ5;
Q1-MAR-2002 (TrEMBLrel. 20, Cz
01-MAR-2002 (TrEMBLrel. 20, La
01-MAR-2004 (TrEMBLrel. 26, La
Hypothetical protein.
                                                                                           -----TEHSIPTP-
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DKELTLPVDSTTLDGSKSSDDQKIISYLWEKTQGPDGVQLENANSSVATVTGLQVGTYVF 362
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RA Wakamatu A., Hayashi K., Sato H., Nagai K., Kimura K., Makitah B., Makamatu M., Dayashi M., Nishi T., Shibahara T., Tanaka T., Tanaka T., Ishii S., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Askine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nagahari K., Ramamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Rahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., RA Takahashi M., Kamibara K., Katanabe M., Hiraoka S., Chiba Y., Ishibashi T., Yamashita H., Murakawa M., Fujimori K., Anani H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishibashi T., Yamashita H., Murakawa M., Fujimori X., Ranehori K., Takahashi-Fuji A., Hara M., Hotuta T., Kusano J., RA Kanehori K., Yanki H., Oshima A., Sasaki N., Aotsuka S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Nomiyama H., Ichihara T., Shiohata N., Sano S., Nomiyama H., Ichihara T., Shiohata N., Sano S., Nomiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Haranabe K., Kumajama A., Takemoto M., Kawakami B., Rumazaki M., Watanabe K., Kumaja A., Takemoto M., Kawakami T., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Robacata A., Hikiji T., Kobacke N., Itakura S., Fukuzumi Y., Anazaki M., Watanabe M., Kobacke N., Inagaki H., Ikamayama K., Pujii Y., Ozaki K., Hirao M., Ohmori Y., Rawakami T., Kobacke N., Inagaki H., Itakanaba M., Sanaki M., Kobata A., Hata H., Watanabe M., Komatsu T., Anterumura K., Nakajamo J., Satoh T., Shirai Y., Takahashi Y., Yamashita R., Kawabata A., Hata H., Watanabe M., Kahabahi Y., Yamashita R., Nakagawa Y., Nakagawa K., Rahashita R., Rawabata A., Hata H., Watanabe M., Kahashil Y., Yamashita R., Kawabata T., Noguchi S., Itoh T., Shigeta K., Yamashita R., Rawabata M., Hata H., Watanabe M., Komatsu T., Kogashi M., Komitani R., Nakagawa Y., Shirai Y., Takahashi Y., Yamashita R., Nakagawa Y., Shirai Y., Takahashi Y., Yamashita R., Nakagawa Y., Shirai Y., Takahashi Y., Ya
                                                                                      CSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKROKRTKIRK
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                                                                                                                                                                   PRKSGLVELTLOVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYV
                                                        RLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVS
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
02-MAR-2001 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein FLJ14225 (FKD1-like protein).
Homo sapiens (Human)
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                                                                                      YIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMDE 1003
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                                                                                                                      332 VKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGHKQ
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01-0C7-2002 (TrEMBLrel. 22, Last sequence update)
01-0R7-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp434C0829 (Fragment).
Name=DKFZp434C0829;
Name=DKFZp434C0829;
Butharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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The German cDNA Consortium;
The German cDNA Consortium;
The German cDNA Consortium;
The German cDNA Consortium;
The German CDNA Consortium;
The German CDNA Consortium;
The German CDNA CONSORTIAN CONSORTIAN
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, AB84315; CAD38985.1;
InterPro; IPR003957; FN III-like.
InterPro; IPR008957; FN III-like.
InterPro; IPR0060601; FN III-
SMART; SM00069; FNS. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        746 AA; 82461 MW; A0945E57D8243191 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50093; PKD; 1.
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989 IRKKTKYTILDNMDEQERMELRP--KYGIKHRSTEHNSSLMVSESEFDSDQDTIFSREKM 1046
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                                                                                                                                                                                                                                                                           GSEGKHVVMQCVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAV 628
  36 IVSYLWTRDEGSPAAGEVLNHSDHHPILFLSNLVEGTYTFHLKVTDAKGESDTDRTTVEV 424
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                                                OPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVILNVLDSDIKVQKIRAHSDLSTVIV
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"Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 8:85-95(2001).
EMBL. ABGSH40: BAB44466.1;
InterPro; IPR003961; FN III.
InterPro; IPR003957; FN III.
InterPro; IPR000601; PKD.
SMART; SM00060; FN3; 3.
SMART; SM00089; PKD; 4.
PROSITE; PS50093; PKD; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2004 (TrEMBLrel. 26, Last annotation update)
KIAA1837 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      639 AA
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62.0%;
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TISSUE-Brain;
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SEQUENCE
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Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hasieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shovchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butrerfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
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Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; BCO31672; AH3167.1; -.
INTERPC; IPR001361; FN III.
INTERPC; IPR000691; FN III-like.
INTERPC; IPR000601; FW
SMART; SM00060; FN3; 3.
                                                                       Genet. 36:40-45(2004)
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Matches 410, Conservative
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Strauberge R.L., Fatnon G.B.A., Grouse L.H., Derge J.G.B.

Strauberge R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strauberge R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rlausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A litschul S.F., Zeeberg B.B., Bardrow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

Rachey J., Helton B., Retteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Generation and initial analysis of more than 15,000 full-length human
                                       YVFTLTVKDERNLGSQSSVNVIVKEEINKPPIAKITGNVVITLPTSTAELDGSKSSDDKG 365
                                                                                                                                            SSKGKVVEMQGVRTPTLQLSAMQEGDYTYQLTVTDT1GQQATAQVTV1VQPENNKPPQAD 245
                                                                                                                              IVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGASDTDTATVEV 808
                                                                                                                                                                                   QPDPRKSGLVELTLQVGVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIV 868
                                                                                                                                                                                                                                                                                          RCICSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKRQKRTK 988
                                                                                                                                                                                                                                                                                                                    604
                                                                          YHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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STRAIN=FVB/N; TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKRQKRTKIRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KELI PPVESATLDGSSSSDDHGI VFYHWEHVRGPSAVEMENI DKAIATVTGLQVGTYHFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 NSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLINGNOSSDDHQIVLYEWSLGPGSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573 KHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIVKDOOGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVSY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days embryo whole body cDNA, RIKEN full-length en
11brary, clone:C430042D23 product:HYPOTHETICAL 103.9 kDa PROTEIN
homolog (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                    603 AA; 65967 MW; BEODA1665D4046BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 3.6e-74; 76; Mismatches 143;
                                                                                                                                                                            IEA.
EMBL, BC022154; AAH22154.1; -.
MGD; MG1:2140475; AUG040320.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007156; P:homophilic cell adhesion; IEXSMART; SM00060; FN3; 2.
SWART; SM00089; PKD; 3.
PROSITE; PS50093; PKD; 1.
NOW TER.
1 1 1
SEQUENCE 603 AA; 65967 MW; BEODA1665D4046BI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.0%; Score 1675.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 59.49
Matches 328; Conservative
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SEQUENCE FROM N.A.
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70 AWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGI 129

SVLWLSTDADESR--CQQGKTLYGAGLRTEGE-NHLRLLAGSLPFHACRAACCRDSACHA 97

130 WGDSPEDIRKDLXFLGKDWGLEE-------MSEYXDDYRELEKDLLQPSGKQEPR 177

98 LWWLEGMCFQADCSKPQSCQPFRTDSSNSML-----

231 ERSVLLPLPTTPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKS 290

KNVSIHPEPS

245

347 320

263

187 --ROKRDLSVVPTHGAMQHSKVNHSEEAGALSPTSAEVRKTITVAGSFTSNHTTQTPEWP

178 GSAEYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELH-----YLNESASTPAPKLP

291 PVLTVTPGSTEHSIPTPPTSAAPSES--TPS-ELPISPTTAPR-TVKELTVSAGDNLIIT 346 LPDNEVELKAFVAPAPAPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFK 406 

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MGD, MGI:2140475, AU040320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUB=Whole body; MEDLINE=10499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Whole body;

STRAIN=C57BL/6J; TISSUE=Whole body;

STRAIN=C57BL/6J; TISSUE=Whole body;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A MEDLINE C57BL/6J; TISSUE=Whole body;

A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsuncto H., Sakaquchi S., Ikegami T., Kashiwagi K., A Yanamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carrinci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A..
STRAIN=CSTBL/61; TISSUE=Whole body;
STRAIN=CSTBL/61; TISSUE=Whole body;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                        SEQUENCE FROM N.A.
STRARIES/PBL/6J; TISSUE-Whole body;
MEDILINE=21.08566; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
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PROSITE; PS50093; PKD; 1.
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380 VIVDGQNAHGEGYVNVTVKPEPRKNRPPVAVVSPQFQEISLPTTSTIIDGSQSTDDDKIV SYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVD YPPVANAGPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLH

467

527

587

VIVSSENAFGEGFVNVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIV

407

499 586 646

SSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTST 706 

LTV 709

620 707

647

VNV 682

560 LSAMQEGDYTYQLTVTDTAGQQATAQVTVIVQPENNKPPQADAGPDKELTLPVDSTTLDG

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LSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKEL1FPVESATLDG

466

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SEQUENCE FROM N.A.
MEDILINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Addams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., RAPILI J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basna A., Baxendale J. Bayrakaraoglu L., Basaley B.M., Beeson K.Y., Bernos P.V., Bernan B.P., Bhandari D., Bolshakov S.M., Berken D.A., Buller H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Daller H., Cadieu E., Davies P., Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rosler C., Gabrielia A., E., Garg M., Bransser K., Bransleilan A. B., Garg M., S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houstron K.A., Howland T.J., Wall M.H., Ibegwam C., Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lasko P., Lei Y., Levitsky A.A., I.J. J., Li.Z., Liang Y., Lin X., Martei B., McIntcoh T.C., McLeed M.P., McPherson D., Lai X., Mattei B., McIntcoh T.C., McLeed M.P., McPherson D., Mount S.M., Moy M., Murphy B., Murphy L., Rargen G., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Raben H., Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Sheng Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wen R., Zhan G., Zhan M., Zhon G., Zhao Q., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zha
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MEDLINE=22446065; PubMed=12537568;

Retal S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Patel D.J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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MEDLINE=22426070; PubMed=12537573;
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"Annotation of the Drosophila melanogaster euchromatic genome: a

3enome Biol. 3:RESEARCH0083-RESEARCH0083(2002)

systematic review

to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2002)

FlyBase

SEQUENCE FROM N.A.

SEQUENCE FROM N.A

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117310 MW; 2BASOA62EEE463DB CRC64;
             the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          ilarity 32.1%; Pred. No. 7.5e-63;
Conservative 172; Mismatches 383;
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FYBases: FBGR0035833; CG7565.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
SMART; SM00181; EGF; 1.
                                                                                                                               PROSITE; PS01186; EGF
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Matches 373; Conserv
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                           1042 SREKMERGNPKVSMNGSIRNG 1062
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Search completed: October 12, 2005, 10:21:38 Job time : 134 secs

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Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1622, Ap	Sequence 11, Appl	Sequence 3, Appli	Sequence 5, Appli	Sequence 8, Appli	Sequence 9, Appli	Sequence 12, Appl	Sequence 259, App	Sequence 273, App	Sequence 274, App	Sequence 7, Appli
SUMMARIES	US-10-408-765A-1622	US-10-764-390-11	US-10-764-390-3	US-10-764-390-5	US-10-764-390-8	US-10-764-390-9	US-10-764-390-12	US-10-764-390-259	US-10-764-390-273	US-10-764-390-274	US-10-764-390-7
DB	16	16	16	16	16	16	16	16	16	16	16
% Query Match Length DB	1072	1072	1072	1072	1072	1072	1072	1072	1053	1053	1063
% Query Match	6.66	99.9	99.9	6.66	6.66	66.66	6.66	6.66	98.3	98.3	98.3
Score	5576	5576	5574	5574	5574	5574	5574	5574	5485	5485	5485
Result No.	-	~	м	4	D	9	7	œ	6	10	11

US-10-764-390-10 US-110-764-390-272 US-110-97-143-16884 US-10-650-763-39353 US-10-550-704-175 US-10-798-512-175 US-10-805-684-110 US-09-759-508B-2 US-10-759-860-133 US-10-75-149-4768 US-10-756-149-4768 US-10-756-149-4768 US-10-97-143-3193 US-10-840-512-155 US-10-97-143-31983 US-10-099-442-126 US-10-099-442-126 US-10-29-386-313-18 US-10-489-695-21 US-10-489-695-22	Sequence 10, Appl Sequence 272, App Sequence 23553, A Sequence 175, App Sequence 175, App Sequence 175, App Sequence 117, App Sequence 113, App Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 20, Appli Sequence 115, App Sequence 1224, App Sequence 1224, App Sequence 1224, App Sequence 1224, App Sequence 1224, App Sequence 31343, A Sequence 3124, App
16 US-10-764.390-272 20 US-11-097.143-16884 18 US-10-450-763-3953 14 US-10-50-704-175 15 US-10-788-512-175 17 US-10-788-512-175 19 US-09-759-5089-2 18 US-10-759-5089-2 18 US-10-759-5089-2 19 US-10-759-5089-2 19 US-10-759-5089-2 19 US-10-656-8978-2 19 US-10-656-149-4768 17 US-10-875-518-11 16 US-10-61-809-2 19 US-10-875-518-12 20 US-11-097-143-1224 15 US-10-282-1224-75177 20 US-11-097-143-3139 14 US-10-282-1224-75177 20 US-10-282-1224-75177 21 US-10-282-1224-75177 22 US-11-097-143-3139 23 US-10-282-1224-75177 24 US-10-282-1224-75177 25 US-10-282-1224-75177 26 US-10-282-1224-75177 27 US-10-489-695-21	Seddictions of the seddiction
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16 US-10-470-390A-18 17 US-10-489-695-22	
17 US-10-489-695-22	equence 18
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15 US-10-203-875-4	equence 4,
15 US-10-297-639-5	Sequence 5, Appli
15 US-10-369-493-10236	equence 10
18 US-10-450-763-44262	44
18 US-10-450-763-54269	equence 54
15 US-10-415-187-5	equence 5,
15 US-10-282-122A-46163	Sequence 46163, A
15 US-10-282-122A-46577	Sequence 46577, A
10 US-09-840-746-20	20
15 US-10-369-493-5784	equence 57
ALIGNMENTS	
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15 US-10-297-63 15 US-10-297-63 18 US-10-450-76 18 US-10-450-76 15 US-10-415-18 15 US-10-282-12 10 US-09-840-74 15 US-10-369-49	1023 1426 1461 1465 1784

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US-10-408-765A-1622

US-10-408-765A-1622

Sequence 1622, Application US/10408765A

Fublication No. US20040101874A1

GENERAL INFORMATION:

APPLICANT: Ghosh, Sounitra S.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

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APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Glenn, Gary W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

FILE REFERENCE: 600088-465

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: Fast SEQ for Windows Version 4.0

SEQ ID NO 1622

LENGTH: 1072

TYPE: PRT

ORGANISM: Homo sapiens

US-10-408-765A-1622

Query Match

Beet Local Similarity 99.7%; Pred. NO. 0;

Matches 1069; Conservative 0; Mismatches 3; Indels 0; Gaps

Matches 1069; Conservative 0; Mismatches 0; Mismatches 0; Matches 1069; LIMPPTGVLSSLLLLVTIAGCARRQCSEGRITYSNAVISPNLETTRIMRVSHTFPVVUCTAA

| HAPPTGVLSSLLLLVTIAGCARRQCSEGRITYSNAVISPNLETTRIMRVSHTFPVVUCTAA

| HAPPTGVLSSLLLLVTIAGCARRQCSEGRITYSNAVISPNLETTRIMRVSHTFPVVUCTAA
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61 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 120

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Conservative
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US-10-764-390-11
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Best Local Simil
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SULT 2 :10-764-390-11 Sequence 11, Application US/10764390 Publication No. US20040214212A1 GENERAL INFORMATION:

APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Jonn J. Perez-Villar
ITILE OF INVENTION: Entiled 254PlD6B Useful in Treatment and Detection of
ITILE OF INVENTION: Cancer
ITILE OF INVENTION: Cancer
ITILE OF INVENTION: Cancer
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT PILING DATE: 2004-01-23
FRIOR APPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: PastSEQ for Windows Version 4.0 ö 180 120 of 61 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 120 180 240 240 300 300 360 360 420 420 480 480 540 9 9 999 720 09 9 KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVWQGVQTPYLHLSAMQEGDYTFQLK VTDSSRQQSTAXVTV1VQPENNRPPVAVAGPDKEL1FPVESATLDGSSSSDDHG1VFYHW EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA EYTDWGIL PGSEGAFNSSVGDSPAVPAETQQDPELHYINESASTPAPKLPERSVLLPLPT EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT EHSIPTPETSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA Gaps ö Length Indels 16; 3; DB Score 5576; DB Pred. No. 0; 0; Mismatches 99.9%; 601 601 661 ò 요 상

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121 LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA 180
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APPLICANT: Adabovits, Aya
APPLICANT: Challica-Eid, Pia M.
APPLICANT: Challica-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
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APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
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APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANTON: Waller
APPLICANTON: WALER
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT APPLICATION NUMBER: US/04-01-23
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH 1072
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Gaps
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LOCATION: 612
OTHER INFORMATION: Xaa = any
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NAME/KEY: VARIANT
LOCATION: 142
OTHER INFORMATION: Xaa
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NAME/KEY: VARIANT
LOCATION: 157
OTHER INFORMATION: Xaa
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ORGANISM: Homo sapiens
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US-10-764-390-3
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Baitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Ghallita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT FILING DATE: 2004-01-23
FRIOR APPLICATION NUMBER: US6/442,526
FRIOR APPLICATION NUMBER: US6/442,526
FRIOR APPLICATION OF CORP.
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99.7%; Pred. No. 0;
ive 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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; Sequence 8, Application US/10764390
; Publication No. US20040214212A1
; GENERAL INFORMATION:
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US-10-764-390-8
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APPLICANT: Agensys. Inc.

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APPLICANT: Adebovits, Aya

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Ge, Wangmao

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                    S-10-764-390-5
Sequence 5, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
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Matches 1069; Conservative
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ORGANISM: Homo sapiens
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Corresponding Proteins
Useful in Treatment and Detection of
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; Pred. No. 0;
0; Mismatches
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Feris, Mary
APPLICANT: Feris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Nucleic Acids and Corres;
TITLE OF INVENTION: Entitled 254PlD6B Useful;
TITLE OF INVENTION: Entitled 254PlD6B Useful;
TITLE OF INVENTION: Entitled 254PlD6B Useful;
TITLE OF INVENTION: Cancer:
FILE REFERENCE: 51158-20081.0
CURRENT APPLICATION NUMBER: USSO/442,526
PRIOR PRILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SEQ ID NOS: 277
SEQ ID NOS: 277
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Best Local Similarity 99.7%;
Matches 1069; Conservative 0
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ORGANISM: Homo sapiens
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> Sequence 9, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION: APPLICANT: Agensys, APPLICANT: Raitano, Arthur B. RESULT 6 US-10-764-390-9

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US-10-764-390-12

i Sequence 12, Application US/10764390

i Publication No. US20040214212A1

GENERAL INFORMATION:

i APPLICANT: Raitano, Arthur B.

APPLICANT: Raitano, Arthur B.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Ge, Wangmao

APPLICANT: Ge, Wangmao

APPLICANT: Steven B. Kanner

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                   LAVLINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF
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Best Local Similarity 99.7%;
Matches 1069; Conservative
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ORGANISM: Homo sapiens
US-10-764-390-12
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                            Sequence 273, Application No. US200; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  -10-764-390-273
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TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection TITLE OF INVENTION: Cancer FILE REFERENCE: 51188-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR PPLICATION NUMBER: US60/442,526
PRIOR PPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
SOFTWARE PASSEQ for Windows Version 4.0
SEQ ID NO 259
LENGTH: 1072
                                                                                                                                                                                                                                                                                                   MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA
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Pred. No. 0;
0; Mismatches
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Matches 1069; Conservative
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US-10-764-390-259
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovite, Aya
APPLICANT: Jakobovite, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT FILING DATE: 2004-01-23
PRIOR PRLING DATE: 2004-01-23
PRIOR PRLING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SSETUL OF 273
FENORMED 1005: 277
FENORMED 1005: 273 1020 1020 840 960 199 180 259 240 319 900 80 VSCPHKENCEPKKNGPIRSYLTFVLRPVORPAQLLDYGDMMLNRGSPGGIWGDSPEDIRK 139 120 300 ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT 379 79 9 901 LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLMMENLIQRYIWDGESNCEWSIFYVT 961 VLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST VSCPHKENCEPKKOMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK DLPFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV GDSPAVPAETQQDPELHYLINESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ 241 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST DLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV SSNSSGKEVIAPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS LAVLLINVLDSDI KVQKI RAHSDLSTVI VFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 20 CARKOCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWFEGRCYL 1 CARKQCSEGRIYSNAVISPNLETIRIMRVSHTPPVVDCTAACCDLSSCDLAWWFEGRCYL GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ Gaps EHNSSLAVSESEPDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 ö Length 1053; Indels DB 16; 3; Score 5485; DB Pred. No. 0; 0; Mismatches 320 ò

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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Butitled 254PlD6B Useful in Treatment and Detection of TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT APPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-01-24
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                                        POLQELTLPLTSALIDGSQSTDDTBIVSYHWBRINGPFIBEKTSVDSPVLRLSNLDPGNY
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Publication No. US20040214212A1
GENERAL INFORMATION:
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US-10-764-390-274
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US-10-764-390-274
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 274
LENGTH: 1053
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Best Local Similarity
Matches 1050; Conserv
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Butiled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-2004.00.23
FILE REPERENCE: 51158-2004.01-23
PRIOR PILLING DATE: 2004.01-23
PRIOR PILLING DATE: 2003.01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 1063
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APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Bid, Pia M.
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ORGANISM: Homo sapiens
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APPLICANT: Relation. Arthur B.
APPLICANT: Allitan-Eid, Pia M.
APPLICANT: Challitan-Eid, Pia M.
APPLICANT: Challitan-Eid, Pia M.
APPLICANT: Challitan-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Geven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Butiled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Butiled 254PlD6B Useful in Treatment and Detection of
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
FRIOR APPLICATION NUMBER: US60/442,526
PRIOR APPLICATION NUMBER: US60/442,526
PRIOR SEQ ID NOS: 277
NUMBER OF SEQ ID NOS: 277
SOFTWARE: PastSEQ for Windows Version 4.0
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99.7%; Pred. No. 0;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION:
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Matches 1050; Conservative
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ORGANISM: Homo sapiens
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1040 IFSREKMERGNPKVSMNGSIRNGASFSYCSKDR
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                                                        RESULT 13
US-10-764-390-272
US-10-764-390-272
Sequence 272, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
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APPLICANT: Agensys, Inc.
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APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
TITLE OF INVENTION: Butiled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT PILING DATE: 2004-01-23
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
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                                                                                                                  TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD
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EXPRESSION OF 10,000 OR
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APPLICANT: veries, v. tais,
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC;
TITLE OP INVENTION: DERARAYS, FOR DETECTING EXPITITE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOO0728
CURRENT APPLICATION NUMBER: uS/11/097,143
CURRENT FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 2000-01-24
PRIOR PILING DATE: 2000-01-24
PRIOR PILING DATE: 2000-01-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-03-3
NUMBER OF SEQ ID NUMBER: 60/194,831
PRIOR PILING DATE: 2000-03-3
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASTSEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 16884
TENNING DATE: 10.00
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Publication No. US20050208558A1
GENERAL INFORMATION:
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ORGANISM: DROSOPHILA
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Query Match 26.0%; Score 1451.5; DB 20; Length 1069; Best Local Similarity 32.1%; Pred. No. 2.3e-80; Matches 373; Conservative 172; Mismatches 383; Indels 233; Gaps
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764 GDVIDGSDHSVALQLINLVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQ
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Job time : 913 secs
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DPLTKRCICSHLWMENLIQRYIWDG-ESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCK
                          ROKRIKIRKKI-KYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDTIF
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Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILE REFERENCE: 790C1P3/US;
CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR PELLICATION NUMBER: 09/640,167

PRIOR PELLICATION NUMBER: 09/649,167

PRIOR APPLICATION NUMBER: 09/649,167
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                                                                                                               1042 SREKMERGNPKVSMNGSIRNG 1062
                                                                                                                                                                                                      ETRTKSNGLGKHKSHNSHSHG 1041
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APPLICANT: Jakobovits, Aya
APPLICANT: Ge, Hangmao
APPLICANT: Ge, Mangmao
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Out J. Perez - Villar
APPLICANT: Duan J. Perez - Villar
APPLICANT: Duan J. Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
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Jakobovits, Aya
Challita-Eid, Pia M.
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Match
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                                                                                                                                            Score
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-MODBLE frame+ pl. n.model - DEV=Xlp
-MODBLE frame+ pl. n.model - DEV=Xlp
-G=/Cgn2 1/USPTO_spool p/US10764390/runat_12102005_110204_22383/app_query.fasta_1.1223
-G=/Cgn2 1/USPTO_spool p/US10764390/runat_12102005_110204_22383/app_query.fasta_1.1223
-D=Published Applications NA - QFMT=fastap_ -SUPFIX=plo.sum62
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human+0 - QFMT=Fastap_START=1 - START=1 - MATRIX=blosum62
-TRR MIN=0 - ALIGN=15 - MODBE-LOCAL_OTTPMT=ptc - NORM=ext - HEAPSTZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10764390 @CGN 1 1 723 @runat_12102005_110204_22383
-NCPUe - LCOPIS - NORM P -LARGEQUERY - NEG SCORES=0 - WAIT -DSPBLOCK=100
-LONGLOG - DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=0.5
-FGAPOP=6 - FGĀPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DBLOP=6 - DELEXT=7
                                                                                                                                                                 ; Search time 3809 Seconds
(without alignments)
1960.176 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/DEGOF_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/PUSOF_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10P_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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6/ptodata/2/pubpna/US10 NEW PUB.seq:*
6/ptodata/2/pubpna/US11A PUBCOMB.seq:*
6/ptodata/2/pubpna/US11 NEW PUB.seq:*
6/ptodata/2/pubpna/US60 NEW PUB.seq:*
6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Sequence 1, Appli Sequence 144, App Sequence 41, Appl Sequence 3, Appli Sequence 2, Appli Sequence 53, Appl Sequence 52, Appl Sequence 29584, A Sequence 39, Appl Sequence 7627, Ap Sequence 20867, score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Sequence 27, Sequence 17, Sequence 10, Sequence 1, Sequence 1, Sequence 10 Sequence 8
Sequence 1
Sequence 1
Sequence 6
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Sequence 8 Sequence Sequence 3 Sequence 3 Sequence 3 Sequence 5 Sequence 5 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 0 US-10-764-390-2 0 US-10-764-390-4 0 US-10-764-390-4 0 US-10-764-390-270 0 US-10-764-390-6 0 US-10-764-390-6 0 US-10-764-390-6 4 US-11-097-143-16883 2 US-10-450-763-8985 4 US-11-097-143-16882 0 US-10-764-390-1 0 US-10-764-390-1 1 US-10-764-390-1 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-78-698-1034 1 US-10-756-149-144 2 US-10-917-384-2 1 US-10-917-384-2 1 US-10-917-384-2 1 US-10-282-122A-3893 4 US-11-097-143-31981 1 US-10-297-639-14 2 US-11-097-143-31981 2 US-10-956-157-1961 2 US-10-956-157-1961 2 US-10-450-763-2984 4 US-11-097-143-31984 2 US-10-450-763-2984 4 US-11-097-143-31981 1 US-10-450-763-2984 4 US-11-097-143-31981 1 US-10-489-695-52 US-09-864-761-20867 US-10-029-386-20814 ALIGNMENTS SUMMARIES B

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	641	Qy 661 GluHisValArgGlyProSerAlaValGluMetGluAsnIleAspLysAlaIleAlaThr 	681 2552	701 2612	721 2672	741 2732	2792	2852	2912	821 ThrLeuglingalGlyGlnLeulinrGluGlarglyBaBpinrLeuvalargGl 	3032	3092	3152	901 3212	921 3272	Oy 941 IleGlnargTyrIleTrpAspGlyGluSerAsnCysGluTrpSerIlePheTyrValThr	3392	Oy 981 CYSLYSARGGINLYSARGINELYSIICARGLYSIYENKINELYSIYENELLEGGGUNSDASH
261 SerAsnSerGluvalLeuMetProSerHisSerLeuProProAlaSerLeu 280 		GluHisSerIleProThrProProThrSerAlaAlaProSerGluSerThrProSerGlu 	LeuprolleSerProThrThrAlaProArgThrValLysGluLeuThrValSerAlaGly	341 AspAsnLeulleIleThrLeuProAspAsnGluValGluLeuLysAlaPheValAlaPro 360 	361 AlaProProValGluThrThrTyrAsnTyrGluTrpAsnLeuIleSerHisProThrAsp 380 	381 TyrGlnGlyGluIleLysGlnGlyHisLysGlnThrLeuAsnLeuSerGlnLeuSerVal 400 	401 GlyLeuTyrValPheLysValThrValSerSerGluAsnAlaPheGlyGluGlyPheVal 420 	421 AsnValThrVallySProAlaArgArgValAsnLeuDroProValAlaValValSerPro 440	441 GlnLeuGlnGluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThr 460 	461 AspaspThrGluIleValSerTyrHisTrpGluGluIleAsnGlyProPheIleGluGlu 480	481 LysThrSerValAspSerProValLeuArgLeuSerAsnLeuAspProGlyAsnTyrSer 500	501 PheArgLeuThrValThrAspSerAspGlyAlaThrAsnSerThrThrAlaAlaLeuIle 520 	521 ValasnasnalavalaspTyrProProValalaasnaladlyProAsnHisThrIleThr 540 		561 LeuTyrGluTrpSerLeuGlyProGlySerGluGlyLy8HisValWalMetGlnGlyVal 580 	581 GlnThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAB9TyrThrPheGlnLeuLy8 600 	valThrAspSerSerArgGlnGlnSerThrAla***valThrValIleValGlnProGlu 	621 AsnAsnArgProProValAlaValAlaGlyProAspLysGluLeuIlePheProValGlu 640

	rgGlySerAla 1
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1234 GACTACTCCATCTTCAGGAGAGGTGTTGGAGAAAGAAAGGCTTCTCAGCTCCAGGAACA 1293
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                                                                                                                                              6797
1069
                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
FRIOR APPLICATION NUMBER: US60/442,526
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 270
LENGTH: 6797
                                                                                                                                                                                                Gaps:
                                                                                                                                             0
5546.50
99.53%
99.53%
20.40%
                                                                                           TYPE: DNA
CRGANISM: Homo sapiens
US-10-764-390-270
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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| Sequence 6, Application US/10764390
| Publication No. US20040214212A1 |
| GENERAL INFORMATION: | APPLICANT: Agensys, Inc. |
| APPLICANT: Adrency Arthur B. |
| APPLICANT: Challita-Eid, Pia M. |
| APPLICANT: Challita-Eid, Pia M. |
| APPLICANT: G. Wangmao |
| APPLICANT: Steven B. Kanner |
| APPLICANT: Steven B. Kanner |
| APPLICANT: Juan J. Perez-Villar |
| APPLICANT: Juan J. Perez-Villar |
| TITLE OF INVENTION: Entitled 254PID6B Useful in Treatment and Detection of |
| TITLE OF INVENTION: Cancer |
| TITLE OF INVENTION: Cancer |
| FILE REFERENCE: 51158-20081.00
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         2914 GGACACAGACACTGCCACTGTGGAAGTGCAGCCAGACCCTAGGAAGAGTGGCCTGGTGGA
                                   uLeuThrLeuGlnValGlyValGlyGlnLeuThrGluGlnArgLy8AspThrLeuValAr
                                              GCTGACCCTGCAGGTTGGTGTTGGCTGACAGAGCAGCGGAAGGACACCCTTGTGAG
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CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: PASLSEQ for Windows Version 4.0
LENGTH: 6991
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US-10-764-390-6
                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE REPERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
FRIOR PELLING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 6991
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 269, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION: APPLICANT: Agensys, Inc. APPLICANT: Raitano, Arthur B.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Venter, J. Craig
APPLICANT: et al.

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PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-11-12
PRIOR PELICATION NUMBER: 60/173,383
PRIOR PILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR PILING DATE: 1999-11-2
PRIOR PILING DATE: 2000-01-2
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR PILING DATE: 2000-01-2
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PILING DATE: 2000-01-2
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASTSEQ FOR WINGOWS VERSION 4.0
FUNDALLY SAFETSED FOR WINGOWS VERSION 4.0
Sequence 16883, Application US/11097143
Publication No. US20050208558A1
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766 2422 786 2482 806 2542 826	Db 2602 ATCTCTGTGG  Qy 846 AsnValLeu  Db 2662 GGAGAT  COY 864 SerThrval:  Db 2716 GCTACTGTGC  QY 884 Gluvalala  :::          Db 2773 CAAGTGGAG  QY 904 LysValLeu  QY 904 LysValLeu  Db 2833 GCAGTG  Db 2893 GCAGTG  Db 2890 AATCCCAT;	944 2944 963 3004 3064 1002	Oy 1022 HisAsnSer;  Db 3139AATTATT  QY 1042 SerArgGlui  Db 3196 GAGACCCGC  QY 1062 Gly 1062  QY 1062 Gly 1062  QY 1062 Gly 1062  Db 3256 GGA 3258  RESULT 8  US-10-450-763-8985  ; Sequence 8985, Applic. ; PILE REFERAL INFORMATION: ; APPLICANT: Hyeeq, In; ; TITLE OF INVENTION: ; FILE REFERENCE: 790C
407 ValThrValSerSerGluAsnAlaPheGlyGluGlyPheValAsnValThrValLys 425 1342 GATCAGAGCAAGTCGAAGCTATCGAATCTTTCGGAGGGACTGTATACTTTTAAG 1341 407 ValThrValSerSerGluAsnAlaPheGlyGluGlyPheValAsnValThrValLys 425 1342 GTCACTGTAACTGGTGACAATGGAACCTTTGGCGAGGCAACAGCTATACAGTGCTT 1401 426 ProAlaArgArgValAsnLeuProProValAlaValValSerProGlnLeuGlnGluLeu 445 1102 CCCGAGAATCAATCAGCCACCACAAGTCATCTGCCCCAGGGAGCAGATCATC 1461 446 ThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThrAspAspThrGluIle 465 11162 CGTCAGCCCACCACAATGCAATTGATGGAGGAGCAGATGATGATGTTACAGTGCCACCACAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGATGATGATGATGATGATGATGATGATGATGATGATG	1522 ACCAATTGGCACTGGAGTGTTTTCGGGACCGATTGGTTACCAACCA	1822 AAGGATGCTAGGCCAAGGCTGTGGATATGCAGAATACAAGAACACCCTATGTT 1881  586 HisLeuSerAlaWetGlnGluGlyAspTyrThrPheGlnLeuLy8ValThrAspSerSer 605  1882 CAGCTGTCCAATTGGAGGAGAGATGTACACTTTTGTTCTAAAAGTAACGATGGCAGT 1941  606 ArgGlnGlnSerThrAla***ValThrValIleValGlnProGluAsnAsnArgProPro 625	666 ProSerAlaValGluMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeuGln 685 2122 CCCAATAATGCAGTCATTTGAAGTCCAACTCATTGCCAATGCCACTCTTGACT 2181 686 ValGlyThrTytHisPheArgLeuThrValLysAspGlnGlnGlyLeuSerSerThrSer 705 2182 CTGGGACTCTATGAGTTCGAATTAACGTAGCTGCTGATGAAATAATAACGCGCACGGAC 2241 706 ThrLeuThrValAlaValLysLysGluAsnAsnSerProProArgAlaArgAlaArgGluC 2241 707 ThrLeuThrValAlaValLysLysGluAsnAsnSerProProArgAlaArgAlaArgGluC 2241 708 ArgHisValLeuDroAsnAsnGGAACGCAGCTCCAATAGCCAACGCCGCGGGT 2301 726 ArgHisValLeuProAsnAsnSerlleThrLeuAspGlySerArgSerThrApp 745 720 GATCACCACCTGCCGGCCACCGCCATCTATTACATGGCTCTAAATCCTGGGAT 2361 746 AspGlnArgIleValSerTyrLeuTrD1leArgAspGlyGlnSerProAlaAlaGlyAsp 765 781 AspGlnArgIleValSerTyrLeuTrD1leArgAspGlyGlnSerProAlaAlaGlyAsp 765 782 GACCTGGCTGTCGAACACTCTGGAACACACACACACACAC
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BARGThriys1leArgiysiyaThr---LysTyrThrileLeuAspAsnMet 1001
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TACCAGAGCCTTGCATATGCGAGGGGTTCTGGATGCCATCG-----GCTGGC 2943
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AGATACCGACAAGGAGCCCGTAATGATTTTGACCAATTTAGTACAAGGCCGC 2481
                                                                                                                                uArgValAspThrAlaGlyCysLeuLeuLysCysSerGlyHisGys 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uThrLysArgCyslleCysSerHisLeuTrpMetGluAsnLeuIleGlnArg 943
odlySerAspHisSerValAlaLeuGlnLeuThrAsnLeuValGluGlyVal 785
                                                        eHisLeuArgValThrAspSerGlnGlyAlaSerAspThrAspThrAlaThr 805
                                                                                                                                                                                                                                                                                           111eValPheTyrValGlnSerArgProProPheLysValLeuLysAlaAla 883
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                                                                                                                 1GlnProAspProArgLysSerGlyLeuValGluLeuThrLeuGlnValGly
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1274 GGCGTGTCATGATCACCATCTGACCATGTG----GCTGTCCTCTCTCTTGTCTCTTC 1330
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                                                                                                                        AspLysAlalleAlaThrValThrGlyLeuGlnValGlyThrTyrHisPheArgLeuThr
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      -- ATTACTTAGGGAGTACAG
                                                         AsnArgProProValAlaValAlaGlyProAspLysGluLeuIlePheProValGluSer
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                                      ThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAspTyrThrPheGlnLeuLysVal
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CTHER INFORMATION: 60% homologous to Homo sapiens dJ73M23.3 (KIAA0319), accession
CTHER INFORMATION: number AL031230, Smith-Waterman Score=1025.
US-10-450-763-8985
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CTTGCATGTTGAACTGTACAACTTTTCTTTATGTTACAGTTGTCCGTCGACTTTATGTC
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-66-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CLUSCOM
SOFTWARE: CLUSCOM
LENGTH: 2423
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| ACTTACTTGTGCTTC-----
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53.20%
47.73%
23.55%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Alignment Scores: Pred. No.: Score: Score: Bercent Similarity: Best Local Similarity: Query Match: DB:	US-10-764-390-3 (1-1072) x US-11-097-143 Qy 8 LeuSerSerLeuLeuLeuValTh	1157	Cy 22	Qy 32 SerAsnAlaVallleSerProAsnLe	Db 1277 GGCGGTTCTATATCGCCCAATT	Oy 52 Phe	Db 1328 TTCGAAAACGCCACTCCGCGGGATGA	Db 1388 CCGCCGGATGCAGTGGAGCCACTGGA	Qy 61 CysCysAspLe	Db 1448 TGCTGCGAAAAGCCCCGGAATGGCAG	76	Db 1508 AAATGCTACCATATCCGATGCCAGACQACQACQACAGACGACAGACGACAGACAGACGAAAAAAAA		Qy 108	Db 1625 CCACAGCTCCTCAAGGCGGAGGCAGG	Qy 119 MetMetLeuAsnArgGlySerProSe	Db 1685 GCGCACTTAAT		Db 1712 AGAAGGTTGAGCTACCTGGCTGCAA	152	1772 CTGACTATTTATTA	Db 1832 GATTTCCCATTGGCCGACAAGGCGAAGGCGAAGGCGAAGGGCGAAGGGCGAAGGCGAAGGGGGG	175	Db 1888	Qy 195 PheAsnSerSerValGlyAspSerP	Db 1889	Oy 215 LeuHisTyrLeuAsnGluSerAla     ::: :::
Qy         922 sCysAspProLeuThrLysArgCysIle	Qy 951 nCysGluTrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLe 969 	969 uThrGlyGlyPheThrTrpLeuCyslle	Db 1649ACCTTTCTAAAGATCTGAGTTGAGTTTTCATTGTTCCTTTCAGACA 1695 Qy 984 nLysArgThrLysIleArgLysLysThrLysTyr 995		Qy 996ThrileLeuAsp 999	Db 1756 TACCCATTGAATTCTAATCCTGCCCATAGCGGTACGAGGTATGTGCAATGATTATCCCCA 1815	Qy 1000AsnMetAspGluGlnGluArgMetGluLeuArgProLysTy 1013	Oy 1013 rGlyjlelysHisArgSerThrGluHisAsnSerSerLeuMerValSerGluSerGluPh 1033	Db 1876 AGGIATCAAGCACCGAAGCACAGAGCACAACTCCAGCCTGATGGIATCCGAGTCTGTGAG 1935		Db 1936 GAGTTTTGACAGGACTGTCTCCCAAAC 1963	RESULT 9 US-11-097-143-16882 ; Sequence 16882, Application US/11097143		; APPLICANT: Venter, J. Craig ; APPLICANT: et al.	; TITLE OF INVENTION: DEFECTION K11, SUCH AS NUCLEIC ACLD ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE . TITLE OF INVENTION. DESCRIPTION OF 10,000 OR MORE	; IIILE OF INVENTION: DECOMPTION GENES. ; FILE REFERENCE: CL000728 · CHERENT ADDITCATION NUMBER IIS/11/097 143	CONTENT FILING DATE: 2005-04-04  PRIOR ADPLICATION NIMBER: 60/157, 832	; PRIOR FILING DATE: 1999-10-05 ; PRIOR APPLICATION NUMBER: 60/160,191	; PRIOR FILING DATE: 1999-10-19 ; PRIOR APPLICATION NUMBER: 60/161,932	; PRIOR FILING DATE: 1999-10-28 ; PRIOR APPLICATION NUMBER: 60/164,769	FILING DATE: 1999-	; FRICK FILING DAIE: 1999-12-28 ; PRIOR APPLICATION UNDER: 60/175,693 : PRIOR FILING DATE: 2000-01-12	APPLICATION NUMBER: 60/184,83 FILING DATE: 2000-02-24	APPLICATION NUMBER FILING DATE: 2000	; NUMBER OF SEQ 1D NOS: 43008 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SOFTWARE: FastSEQ for Windows Version 4.0	; SEV ID NO 18882 ; TEMPH: 5775 . TVDE: NA	, ORGANISM: DROSOPHILA US-11-097-143-16882

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|VTGCGGATGTCGTCAGCATATGCCGACGTCACAACG 1216
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------GATGTTCTGGCCAACGAGAG 1909
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ATGGTACTGGTCATGGTCCACATGG 1624
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AATCAGGTAATAGCATATTGGTTTCTCTCTATATTC 1771
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                                                                                                                                                                                                                                                  ----ArgiysGlnCysSerGluGlyArgThrTyr 31
                                                                                                                                                                                                                                                                                                                                                                                                            -----CysThrAlaAla 60
                                                                                                                                                                          thrileAlaGlyCysAla----- 21
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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3608 3668 CAATCGAGTACAGCTAAGGTCCATGTGTTTGTGAAGCCTCCCACGAATTCTCCACCAGTT 3070 3131 TATGATCTGTGTTACAGACTACTAGC-TTGCCCATTAATTGGGTTCTTTTGAATGGCTCC 3189 :::||||||| :::::::
8250 AATGCAGTCATTITGAAGTCCAACTCATCAGTAAGTGCATATATATATATATGTTG 3309 GACCTCATGCAACTCCATTTAACCCTGCAGATTGCCAATGCCACTCTCTGACTCTGGGA 3369 3071 GCTGAGGCAGGAAGTAATACGGTAGGTTTCAGTTAAAAGATTATATTTTATTTCGTTTTAA 3130 crcrargagricgaarraacceragegergargaaaaraaraacaccecracecacacacace 3429 3430 TGGGTGAAGATAGT-TCAAGGTAATCATATCCATAATCTTCAGTAGCTCATAGGTGCTAA 3488 746 GTGGCAGATACCGACAA-GGAGCCCGTAATGATTGTGAGTTAAGATTTAACTCTAATCCC 3727 3728 ACTGCGACTIATATTATATACAATTTTCCAGTTGACCAATTTAGTACAAGGCCGCTAT 3787 908 687 ThrTyrHisPheArgLeuThrValLysAspGlnGlnGlyLeuSerSerThrSerThrLeu 707 GluvalGlnProAspProArgLysSerGlyLeuValGluLeuThrLeuGlnValGlyVal 826 GlyGlnLeuThrGluGlnArgLysAspThrLeuValArgGlnLeuAlaValLeuLeuAsn 846 GlnArglleValSerTyrLeuTrplleArgAspGlyGlnSerProAlaAlaGlyAspVal GlyProGlySerGluGlyLysHisValValMetGlnGlyValGlnThrProTyrLeuHis SerSerSerAspAspHisGly1leValPheTyrHisTrpGluHisValArgGlyPro------GluAsnAsnSerProProArgAlaArgAlaGlyGlyArg creecreregreaerarcreregacaceceaceacacacacrarregeaegeaceacr ThrpheHisLeuArgValThrAspSerGlnGlyAlaSerAspThrAspThrAlaThrVal LeuSerAlaMetGlnGluGlyAspTyrThrPheGlnLeuLysValThrAspSerSerArg HisValLeuValLeuProAsnAsnSerIleThrLeuAspGlySerArgSerThrAspAsp ------AsnIleAspLysAlaIleAlaThrValThrGlyLeuGlnValGly ---ValAlaLeuGlnLeuThrAsnLeuValGluGlyValTyr GlnGlnSerThrAla\*\*\*ValThrValIleValGlnProGluAsnAsnArgProProVal ------LysGluLeullePheProValGluSerAlaThrLeuAspGlySer ThrvalAlavalLysLys-------IleAspGlySerAspHisSer------AlaValAlaGlyProAsp-----SerAlaValGluMetGlu------

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1.74e-23
403.00
67.57%
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                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-10-764-390-1
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-764-390-1/c

Sequence 1, Application US/10764390

Publication No. US20040214212A1

GENERAL INFORMATION:

APPLICANT: Raitano, Arthur B.

APPLICANT: Raitano, Arthur B.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Ge, Wangmao

APPLICANT: Ge, Wangmao

APPLICANT: Steven B. Kanner

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1029 SerGluSerGluPheAspSerAspGlnAspThrIlePheSerArgGluLysMetGluArg 1048
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                                                                                                                                                                                                                                                                                                                                              4195
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                                                4021
                                                                                                                       941 IleGlnArgTyrIleTrpAspGlyGluSerAsnCysGluTrpSerIlePheTyrValThr 960
                                                                                             865 ThrValIleValPheTyrValGlnSerArgProProPheLysValLeuLysAlaAlaGlu 884
                                                                                                                                                                                              885 ValAlaArgAsnLeuHisMetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLys 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            938 -----GluAsnLeu 940
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847 ValLeuAspSerAspIleLysValGlnLysIleArg-----AlaHisSerAspLeuSer 864
                                                                                                                                                                                                                                                                                                                          #139 GTG---GAIATITCGCACCTCTGTTTGCCAGAGTGATTGCTCCGGTCATGGGTCGTGAAT
                         3968 GAT---GAGAATAAGATCCAGGTCAGGGAGCTAAAATATGACTTGCATACGAT---GCT
                                                                                                                                                                                                                                                                                              905 ValleuArgValAspThrAlaGlyCysLeuLeuLysCysSerGlyHisGlyHisCysAsp
                                                                                                                                                                                                                                           4079 GIGGAGCGCAGITGAGAACCCAACIGCAGAAGGAIGCATCIAIACIGGGCGCATIIGCA
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282 CACGTCAGAGGCCCCAGTGCAGTGGAGATGGAAAATATTGACAAAGCAATAGCCACTGTG
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; Sequence 68, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Slonim, Donna K.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMOF
; FILE REPREMENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/429,782
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR APPLICATION NUMBER: US 60/427,982
; RRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; TENNYMER: PatentIn version 3.2
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 284
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1014 GlyileLysHisArgSerThrGluHisAsnSerSerLeuMetValSerGluSerGluPhe 1033
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                                                                                                                       943 ArgTyrIleTrpAspGlyGluSerAsnCysGluTrpSerIlePheTyrValThrValLeu 962
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Matches:
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FILE REFERENCE: P2039P1
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US/09/684,524
PRIOR PILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: PCT/US00/08979
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/130,991
PRIOR APPLICATION NUMBER: 60/130,991
PRIOR APPLICATION NUMBER: 60/130,991
PRIOR FILING DATE: 1999-04-26
NUMBER: OF SEQ ID NOS: 344
SOFTWARE: PATENTIN VET. 2.0
SEG ID NOS: 344
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Sequence 89, Application US/107;
Publication No. US2040152164A1
GENERAL INFORMATION:
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                                                             ProProValAlaValValSerProGlnLeuGlnGluLeuThrLeuProLeuThrSerAla 452
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FILE REFERENCE: PS039P1
FILE REFERENCE: PS039P1
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
FRIOR PILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR PILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-09
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; ORGANISM: Homo sapiens
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FILING DATE: 2000-10-23
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA-034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 GGCATCAAACAGAAAGGCCTTTTGCTAAGTAGCAGCCTGATGCACTCCGAGTCAGAGCTG
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Sequence 13443, Application US/10282122A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Malonc, Cheryl
APPLICANT: Malonc, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Kari
APPLICANT: 2yskind, Undith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/203
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
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Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-13443
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PRIOR APPLICATION NUMBER: 60/253,625
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:::     ::: :::     339 aProProProProprogrammer 2072  339 aProAlaproProValGluThrTyrAsmTyrGargagagagagagagagagagagagagagagagagaga	2073 CGTCGCGAGCCAGCGTTGAACAGACCTATGCGCTGGACGGAGCGGGAGCCGCCGCCCGGC 2132 379 TASPTYTGINGlYGlulleLySGInglyHisLySGInThrLeuAsnLe 395 2133 GGACGAAAAGCTGACCTATAAATGGCGTGTGGCGATGCGGATCGTTCGGCATTCGCAATGC 2192		415 eGlyGluGlyPheValAsnValThrValLysProAlaArgArgVa 430 	430 lAsnLeuProProValAlaValSerProGlnLeuGlnGluLeuThrLeuProLeuTh 450	450	468	471 uGlulleAsnGlyProPhelleGluGluLysThrSerValAspSerProValLeuArgLe	491 uSerAsnLeuAspProGlyAsnTyrSerPheArgLeuThrValThrAspSerAspGly		2558 COGANGCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCACAGCACAGCACAGCACAGCACAGCAACAGCAG	546 eThrLeuAsnGlyAsnGlnSerSerAspAspHisGlnIleValLeuTyrGluTrpSe 2658 TCCGCTCGCCAAGTCGCAACTCGCAACCGGAAGGGCAACCGGAAGTGGCG		576 lMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMetGlnGlyAspTyrTh 596   :::    2778 ACCGAAGGCACCACCGGCACGGCGT 2804	596 rPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThrAla***ValTh 614	614 rValileValGlnProGluAsnArgProProValAlaValAlaGlyProAspLysGl 634	634 uLeullePheProValGluSerAlaThrLeuAspGlySerSerSerAsp 651
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rccGGTTGACGGCGCTGCCAA 3323
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                        -GluHisValArgGlyProSe 667
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41984 AAAGACATTAGACCATCAGATATCACTCAGATAACTTCAACCCCAACATCTTCCATGCTT 42043		365 GluThrThrTyrAsnTyr 370     42224 GAAGATGGCGGCTCACCAATTAAGTCCTAATATACTTGAAAAGAGAGAAACCAGCCGACTT 42283	371 GlufrpäsnLeulleSerHisProfhraspfyrGlnGlyGlu 384	385 IleLysGlnGlyHisLysGlnThrLeuAsnLeuSerGlnLeuSerValGlyLeuTyrVal 404 :::       ::: 42338 CTTATCCAAGGAAATGAGTACATC 42361	405 PheLygValThrValSerSerGluAsnAlaPheGlyGluGlyPheValAsnValThrVal 424	425 LysProAlaArgValAsnLeuProProValAlaValValSerProGlnLeu 442 	443 GlnGluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThrAspAsp 462	463ThrGlulleValSerTyrHisTrpGluGlulleAsnGlyProPheIleGluGlu 480 :::	481 LysThrSerValaspSerProVal	497 GlyasnTyrSerPheArgLeuThrValThrAspSerAspGlyAlaThrAsn 513    ::          ::: 42647 GGAGCACCTACGAATTCCGTGTCAGTGCAGAAAAAAAGAGAAGAAGAAATTGGTCCACCCAGT 42706	514 SerThrThralaalaLeuileValasnahaNalaValAspTyrProProValalaAsnAla 533	534 GlyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGlyAsnGlnSer 553	554 Serasp	564Trp 564	565	573 LyshisValvalMetGlnGlyValGlnThrProTyrLeuHis 586 ::: 43004 GAGCCAGCGGTGATTCCAGATGTTGAAATCGTAGAACGGGGGGGTGGTTCTGAA 43063
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Sequence 827, Application US/09270767

Sequence 827, Application US/09270767

Sequence 827, Application US/09270767

Patent No. 6703491

TITLE OF INFORMATION:

TITLE OF INFORMATION NUMBER: 05/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 827
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US-09-903-469-7
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US-09-270-767-827
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-MODEL=frame+ p.D. model - DEV=xlp
-MODEL=frame+ p.Dr. model - DEV=xlp
-MODEL=frame+ p.Dr. model - DEV=xlp
-DS=/2012_1/USPTO_spool_p/US10764390/runat_12102005_110204_22353/app_query.fasta_1.1223
-DS=/2012_1/USPTO_spool_p/US10764390/runat_12102005_110204_22353/app_query.fasta_1.1223
-DS=/2012_1/USPTO_spool_p/US10764390-STRT=1 - SND=-1 - MATRIX=blosum62 - TRANS=bluman40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15
-MODES=LOCAL.OUTFMT=pct - NORM=ext - HEAPEJZE=500 - MINLEN=0 - MAXLEN=200000000
-USER=US10764390 @CGN 1 1 105 @runat_11102005_110204_22353 - NCPU=6 - ICPU=3
-NO_WMAP - LARGEQUERY - NEG_SCORES=0 - WAIT - DSPBLOCK=100 - LONGLOG
-DSW TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 16109, A
Sequence 484, App
Sequence 2590, Ap
Sequence 6552, Ap
Sequence 6552, Ap
Sequence 3204, Ap
Sequence 1013, Ap
Sequence 1013, Ap
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1: /cgn2_6/prodateal/lina/5A_COMB.seq:*

2: /cgn2_6/prodateal/lina/6B_COMB.seq:*

3: /cgn2_6/prodateal/lina/6B_COMB.seq:*

4: /cgn2_6/prodateal/lina/6B_COMB.seq:*

5: /cgn2_6/prodateal/lina/PCTUS_COMB.seq:*

6: /cgn2_6/prodateal/lina/backfiles1.seq:*
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Compugen Ltd
                                                                                                          nucleic search, using frame_plus_p2n model
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Sequence 484, Application US/09902540
; Sequence 484, Application US/09902540
; Patent No. 6833447;
; GENERAL INFORMATION:
APPLICANT: Glodman, Barry S.
; APPLICANT: Glater, Steven C.
; APPLICANT: Misgand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof;
FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 484
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GlyAspTyrThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThrAla*** 612
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                                                        SerSerAspAspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySerGluGly
                                                                                                                        LysHisValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMetGlnGlu
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                                                                                              GCCGGCGATGCCGTGATCTTGTATTTGCCCAAAAAATGTCACTCTGAATGGCACAGCC 312
                                                                                                                                                                  311 AGTTCGGATGATCACGAGATCGTTGCTTGGGACCGAGGATGCTAGCGACGAGGACC 252
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US-09-270-767-16109/C
US-09-270-767-16109/C
Sequence 16109, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
FAPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16109
LENGTH: 553
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                                                                         AlaglyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGlyAsnGln
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                                                                                             3372 GCGGGACCGTCCCCTCTCCGCGTCCGAGGGTGCG-----CAGGTGACGTTCCGC
            lyProAspLysGluLeullePheProValGluSerAlaThrLeuAspGlySerSerSerS
                                         erAspAspHisGlyIleValPheTyrHis-TrpGluHisValArgGlyProSerAlaVal
                                                                                GluMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeuGlnVal-----
                                                                                                                        GlyThrTyrHisPheArgLeuThrValLysAspGlnGlnGlyLeuSerThr---Ser
                                                                                                                                                                ThrLeuThrValAlaValLysLysGluAsnAsnSerPro-----ProArg----
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2590, Application US/09902540
; Sequence 2590, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
APPLICANT: Goldman Barry S.
APPLICANT: Glater, Gregory J.
APPLICANT: Misgand, Noger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses;
FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2590
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Mismatches:
Indels:
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US-09-902-540-2590
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US-09-902-540-2590
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                                                                                               ------SerGlyLysGluValLeuMetProSerHisSerLeuProProAla
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                                                                    AlaGluThrGlnGlnAspProGluLeuHisTyrLeu
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; ORGANISM: Myxococcus xanthus
US-09-902-540-1119
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Patent No. 683347

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Mysococcus xanthus Genome Sequences and Uses Thereof;
FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825
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3625 CCGAGCAACACTGCTCCGGAAGCGGACGCGGGCGAGTCG---GCCATCGTGGCGAGGGC 3681
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                          493 AsnLeuAspProGlyAsnTyrSer----
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US-09-902-540-1119
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LENGTH: 16584
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Best Local Similarity:
Query Match:
DB:
Alignment Scores:
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LysProAlaArgArgValAsnLeuProProValAlaValValSerProGlnLeuGlnGlu 444
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                                                                                         ---ThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAspTyrThrPheGlnLeuLys
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                                                          1483 AACTCTGCGCCGACCGTGAACGCGGCATCGATGCCACGCGAACGCTGGTGACGTCGTG
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                                                                                                                      IleAsnGlyProPheIleGluGluLysThrSerValAspSerProValLeuArgLeuSer
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US-09-902-540-6552 Sequence 6552, Application US/09902540 ; Patent No. 683347 ; GENERAL INPORMATION:

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    ProAsnLeuGluThrThrArg

APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6552
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304
284
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Mismatches:
Indels:
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eulleSerHisProThrAspTyrGlnGlyGlulleLysGlnGly
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NEFAL INFORMATION:
PPLICANT: Keith Weinstock et al
ITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
ITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
ITLE REPRESENCE: 107196.132
URRENT APPLICATION NUMBER: US/09/248,796A
URRENT PILING DATE: 1999-02-12
                                    ||||| ||| ::::::::: |||:::|||:::|||:::|||2759 GCGACCCCGGACGGAGCGTCCCGGTC 2809
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NIOR APPLICATION NUMBER: US 60/074,725
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Mismatches:
Indels:
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Matches:
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 3204
LENGTH: 2481
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215.50
32.80%
22.47%
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Best Local Similarity:
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patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Megand, Roger C.

TITLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

LENGTH: 1119

TYPE: DNA
                                                                          2208 GGTGGTTCCTACCAATTCTGAACTTAGCTCAACTGTTACTGGTAGTTCTGAAACTGCTGC 2267
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2322 AGTTACTGGTAGTGAATGAATTTTGACTGGTAATACTGAAAGAAGTGCTACTGCTATTGC 2381
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                                                            594 pTyrThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThrAla***ValTh 614
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                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                  2.34e-09
207.50
41.40%
25.54%
3.72%
, ORGANISM: Myxococcus xanthus JS-09-902-540-2872
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Best Local Similarity:
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10229 AGCTTCACCGCGCCCGCGGTCGCCAAGGGGAGGCGCGAAGCTCGTCTTCCAGCTCGTGTG 10170
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697 AspGlnGlnGlyLeuSerSerThrSerThrLeuThrValAlaValLys-----Ly
                                               TyrProProValAlaAsnAlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIle
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STRET: 1 South Pinckney Street
STATE: MI
COUNTRY: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
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TITLE OF INVENTION: No. 6365723el Sequences of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
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                          CAGTICACCGCGCCTGAGGTCTCAGCCGCAACGGAGTTCGTCTTCGTGGTGAAGGTCTCC 954
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, ROGER C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFREENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILLING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1013
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   ThrvalThrGlyLeuGlnValGlyThr -----TyrHisPheArgLeuThrValLys
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Sequence 1013, Application US/09902540
Patent No. 6833447
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, ORGANISM: Myxococcus xanthus
US-09-902-540-1013
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APPLICANT: Goldman, Barry S.
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Query Match:
DB:
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|5745 GTTGATCTCACCGCCGTCGCCATCAGCATGAACAGCATCACCAGCGATGATGAGTTAAC 15804
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                                                  363 ProvalGluThrThrTyrAsnTyrGlu---TrpAsnLeulleSerHisProThrAspTyr
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                                                            FILING DATE: 03-Dec-1999
CLASSIFICATION: 4Unknown>
PRIOR APPLICATION: 4Unknown>
PRIOR APPLICATION DATE: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELECHMANICATION INFORMATION:
TELECHMANICATION 10FORMATION:
TELECHMANICATION 10FORMATION:
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TELECHMANICATION 10FORMATION:
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Matches:
Conservative:
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Indels:
                                                  APPLICATION NUMBER: US/09/453,702B
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORD PERFECT 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
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34.40%
20.85%
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Best Local Similarity:
Query Match:
DB:
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ON: (98266)..(98266)
INFORMATION: n equals a,
                                                                                                                                                                                                                                              ION: (98343)..(98343)
INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                      YEY: misc_feature
FION: (191989)..(191989)
R INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /KEY: misc_feature
TION: (224187)...(234187)
R INFORMATION: n equals a,
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R INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                             KEY: misc feature
ION: (103998)..(103998)
INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                       KEY: misc feature
ION: (148948)..(148948)
INFORMATION: n equals a,
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ION: (163385)..(163385)
INFORMATION: n equals a,
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ON: (191995)..(191995)
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
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CON: (559167)..(559167)
INFORMATION: n equals a,
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JOCATION: (622708)..(622708)
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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INFORMATION: n equals
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INFORMATION: n equals
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APPLICANT: Bult et al.
APPLICANT: Bult et al.
APPLICANT: Bult et al.
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: jannaschii
FILE REFRENCE: P8275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
                                                                                               16789 AAAGGCTACAGCGCCACCATTCAGAGCAACGGGAGCTGGAGCGTGAACGTGCCTGCGGCG 16848
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                                              16444 ACGGGGGGGGGGGGGGCGCCTGGTGGTGACCATCGCCGGGCAGTATGTCACC 16503
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                           645 AspGlySerSerSerAspAspHisGlyIleValPheTyrHisTrpGluHisValArg 664
                                                                                                                                                                                         665 GlyProSerAlaValGluMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeu
                                                                                                                                     685 GlnValGlyThrTyrHisPheArgLeuThrValLysAspGlnGlnGlyLeuSerSerThr
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LOCATION: (84773). (84773)
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LOCATION: (28257). (28258)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a,
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|||::: ||| 33829 GGAAATATAGAGGTTGGAATTCCA---CCACCAATTGGAGTTGGAGGATACAGCAGTTAT 33773 33502 ATTTATCCA-----AATCCTGCAAGTTATAAAGATACAATTTCCTTTAGTCCA 33455 33394 TTAATAGGGTATTATCCTATATCTCCCAACCCATGGCAAGAATATATGGATTTAAC 33335 33334 TTAACAGTTTATGATTCTAATGGAAATGTTGCATGGAAT-TACTCATCAAATGAATTAAC 33276 33230 GGTAGTTTGGGÅTGGAATGGGÅGGAGTTÅÅTTCAÅCÅÄCTGTTAAGTTTTAGTGTG---- 33176 33562 GCAGAAAATATGAAAACAGTATATĠTÅATAGACAATAAAAACCĊÀATAGCCAAACTCTAT 33503 33231 431 449 483 298 GlySerThrGluHisSerIleProThrProProThrSerAlaAlaProSerGluSerThr 317 318 ProSerGluLeuProlleSerProThrThrAlaProArgThrValLysGluLeuThrVal 337 338 SeralaGlyAspAsnLeullelleThrLeuProAspAsnGluValGluLeuLysAlaPhe 357 358 ValAlaProAlaProProValGluThrThrTyrAsnTyrGluTrpAsnLeulleSerHis 377 450 ------ThrSerAlaLeuileAspGlySerGlnSerThrAspAspThrGlu-- 464 503 503 uThrValThrAspSerAspGlyAlaThrAsnSerThrThrAlaAlaLeuIleValAsnAs 523 536 556 pHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySerGluGlyLysHisValVa 576 392 ThrLeuAsnLeuSerGlnLeuSerValGlyLeuTyrValPheLysValThrValSerSer 483 rValAspSerProValLeuArgLeuSerAsnLeuAspProGlyAsnTyrSerPheArgLe 33275 TATTATATATCC------AAAAGTTTTCCTATAGGAATTACACTGCTAAATT 378 ProThrAspTyrGlnGlyGlu-------ileLyg---GlnGlyHisLysGln 412 GluAsnAlaPheGlyGluGlyPheValAsnValThrValLysProAlaArgArgValAsn LeuProProValAlaValValSerPro-GlnLeuGlnGluLeuThrLeuProLeu----------lleAsnGlyProPheIleGluLysThrSe --AsnAlaGlyProAs 536 nHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGlyAsnGlnSerSerAspAs -----IleValSerTyrHisTrpGluGlu-----reaggatgtagaattcgttttcccagicitatgacccggagggt--US-10-764-390-3 (1-1072) x US-08-916-421B-1 (1-1664976) Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 33718 ACA------523 nAlaValAspTyrProProValAla-----201.00 35.63**\$** 22.57**\$** 3.60**\$** Score:
Percent Similarity:
Best Local Similarity:
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DB: Alignment Scores: Pred. No.: US-08-916-421B-1 432 465 33175 33119 33673 g g ద g g g & g g a 임 장. 원 g Š δ ò ò ò ò ò Š જે ð g ⋩ ò 셤 ठे ð

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LOCATION: (163385)..(163385)
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APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6797466
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PEZSCI
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/916,421
PRIOR FILING DATE: 1996-08-22
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
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; Patent No. 6797466
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33718 ACA-----ATA 33713 298 GlySerThrGluHisSerIleProThrProProThrSerAlaAlaProSerGluSerThr 317 318 ProSerGluLeuProlleSerProThrThrAlaProArgThrValLysGluLeuThrVal 337 338 SerAlaGlyAspAsnLeuIleIleThrLeuProAspAsnGluValGluLeuLysAlaPhe 357 358 ValAlaProAlaProProValGluThrThrTyrAsnTyrGluTrpAsnLeuIleSerHis 377 378 ProThrAspTyrGlnGlyGlu------ileLys---GlnGlyHisLysGln 391 392 ThrLeuAsnLeuSerClnLeuSerValGlyLeuTyrValPheLysValThrValSerSer 411 33712 GTAGAGCCGCCA-----TCGTGGACTTGGTATTGCCATCATATA----1664976 128 74 217 149 Length:
Matches:
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Indels: US-10-764-390-3 (1-1072) x US-09-692-570-1 (1-1664976) b Þ ρ ρ b c, or g ö ö 9 ö ö ò ö ö ΰ ϋ ΰ ΰ ΰ ວັ ΰ NAME/KEY: misc feature LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a, t, ت FEATURE:
NAME/KEY: misc feature
LOCATION: (1130891)..(1130891)
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LOCATION: (1004830). (1084830)
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LOCATION: (1119881). (1119881) NAME/KEY: misc feature LOCATION: (1349473)..(1349473) OTHER INFORMATION: n equals a, 0.00462 201.00 35.63% 22.57% 3.60% LOCATION: (779676)..(779676) OTHER INFORMATION: n equals Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Mysococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B CURRENT APPLICATION NUMBER: US/09/902,540
                                                                                                         ySerAspHisSerValAlaLeuGlnLeuThrAsnLeuVal-------
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                                              eValSerTyrLeuTrpIleArgAspGlyGlnSerProAlaAlaGlyAspValIleAspGl
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US-09-621-976-13082
Sequence 13082. Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR.2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOSTWARE: PATENT.PM
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Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
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LENGTH: 320
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; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1136
; LENGTH: 16047
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1136
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197.50
32.48%
21.59%
3.54%
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Query Match:
DB:
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APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15512
164
100
243
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38
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                     ZIP: 99352
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
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                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word Processor (WordPerfect 5.1) CURRENT APPLICATION DATA:
                                                                                                                          Paul W. Zimmerman
Intellectual Property Servic
Battelle Memorial Institute
PNNL P.O. Box 999
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STRANDEDNESS: double stranded
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                       ADDRESSEE: PNNL P.O. BOX
STREET: Washington Way
CITY: Richland
STATE: Washington
COUNTRY: U.S.A.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15512 bases
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                  GENERAL INFORMATION:
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US-08-853-659A-5
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                               oValAlaAsnAlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAs 549
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1858 CACGCGGAACCAGCCGTAGGCTACTTCTTGTGCTGCATCGCCGAGGCGATCAGGT 4801
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US-08-853-659A-5
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130043K22 product:hypothetical PKD domain containing protein, full insert sequence.
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High-efficiency full-length cDNA cloning
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-Q=/cgn2 1/08FPO spool pylv310*742*p2n.rst -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
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/strain="C57BL/6J"
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/db xref="raxOn1090"
/clone="D130043K22"
/tissue type="spinal ganglion"
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/dev stage="l2 days embryo"
/dev stage="l2 days embryo"
/note="hypothetical PKD domain containing protein
(InterPro] IPR000601, evidence: InterPro)
putative"
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-rese@gsc.riken.jp, Pax:81-45-503-9216)
CURL:http://genome.gsc.riken.jp/, Tel:81-45-503-922, Pax:81-45-503-9216)
CURA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                  Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramcto, K., Hiradoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Natanyama, T., Myazaki, M., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakazume, N., Sano, H., Sagaki, D., Shibata, K., Shinagawa, A., Shizaki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toyauri, A., Toya, T., Yasunishi, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                           The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 4828)
                                                                                                                                                               The RIKEN Genome Exploration Research Group Phase II Team and the
.o.meda,r., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                a full-length mouse cDNA collection
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Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Functional annotation of a
Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   797
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MetalaProProThrGlyValLeuSerSerLeuLeuLeuLeuValThrIleAlaGlyCys
                       438 IGCTGTGACTTGCTCACCTGTGACCTGGCCTGGTGGTTTGAGGGCAGCTGCTATCTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GluLeuHisTyrLeuAsnGluSerAlaSerThrProAlaProLysLeuProGlu
                                                                                                                                                                             GluThrThrArgIleMetArgValSerHisThrPheProValValAspCysThrAlaAla
                                                                                                                                                                                                                         378 GAAACCATCAGAATCATGCGGGTGTCTCAAACCTTCTCCGTGGGAGACTGCACGGCCGCT
                                                                                                                                                                                                                                                                   CysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuVal
                                                                                                                                                                                                                                                                                                                                                            SerCysProHisLysGluAsnCysGluProLysLysMetGlyProIleArgSerTyrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrPheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMet
                                                                                    21 AlaArgLysGlnCysSerGluGlyArgThrTyrSerAsnAlaValileSerProAsnLeu
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/db xref="GI:26351215"
/trānslation="MEKGLGVKPSPASWVLPGYCWQTSVKLPRSLYLLYSFFCFSVLM
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VOLDEDGENGEWSVLYVIIASFVIVVALGIISHTTIOCCKOKOKRFKKSKTKILDA
TDOBSILEIKPTSRASKOKOFILSSILMESSELDSDDAIFTRPPDREKGKLLAHWCR
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Strain=C57BL/6J"

db_xref="FANTON DB:D330027H07"

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/tissue type="heart"
/clone_lbp=RIKEN full-length enriched mouse cDNA library"
                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 AGCGTTCTGTGGTTGTCAACAGATGCTGATGAGAGCAGA-----TGCCAACAGGGAAG 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="13 days embryo" 100. 3357 / dev_erunamed protein product; HYPOTHETICAL 103.9 KDA PROTEIN homolog [Homo sapiens] (SPTR AALS5781, evidence: FASTY, 85.5%ID, 97.4%length, match=2763)
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524
138
295
109
                                                                                                                                                                      prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330027H07 product:HYPOTHETICAL 103.9 KDA PROTEIN MONOLOG [Homo sapiens], full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
wheth. Enzymol. 303, 19-44 (1999)
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKRN), iBboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 219-0045, Japan (E-mail:genome-res@gsc.riken.jp,
WRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Please visit our web site for further details.
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Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730047D20 product:HYPOTHETICAL 103.9 PROTEIN homolog [Homo sapiens], full insert sequence.
                                  847 lLeuAspSerAspIleLysValGlnLysIleArgAlaHisSerAspLeuSerThrValIl
                                                                                                                                                                                                                                                                                                                                                                                                      2619 GTTGTTTTTTTGTTCAGAACGACCTCCCCAGCTCTTCAAAGGCCATGAGGTGGCAGC
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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GWCPADACSKROSCOPPRIDSSNSMLIFORSPROACHDGLLPEDDSPHLLRLAGRGRTS
GWCPADACSKOGPPRIDSSNSMLIFORDLSVYPTHGAMORSKYNHSEEAGALSPT
SAEVRKTITVAGSFTSNHTTQTPEWPKNYSIHPEPSBHSSPVSGTPQVKSTEHSPTDA
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ARPGETYTYDWQLITHPTDYSGEVBKKISQSLQLSKLTPGLYSTRINGOLNAFVLPE
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NQVTTLPQNSITLEGNGSTDDHGITSYEWSLSPSSKKTVEMQCYSTPLLOGSANDG
DYTYQLTYDTAGQQATAQVTVIVQPENNPEPQADAGPDKELITVVDENRALOGSKSTD
DQRVVSYLWEGSREPDGAQDAGAGVENANSSVATYTGLQVGTYVFTTLVDENRALOGSKSTD
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                                    /note="unnamed protein product; HYPOTHETICAL 103.9 KDA PROTEIN homolog [Homo sapiens] (SPTR|AAL55781, evidence: FASTY, 85.5%ID, 97.4%length, match=2763)
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_stage="7 days neonate"
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Qin, W.X., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Huang, Y., Zhao, X.T.
Wan, D.F. and Gu, J.R.
Novel human cDNA clones with function of inhibiting cancer cell
                                         2724 GTTGTTTTTTGTTCAGAACGACCCCCCACCAGCTCTTCAAAGGCCATGAGGTGGCAGC
                                                                                         gAsnLeuHisMetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysValLeuAr
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/clone="pp791"
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayahida, K., Hayatau, N., Hirozame, T., Harai, F., Hirozame, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, S., Sagobe, Y., Tangami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tangami, M., Toyawa, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Direct Submission
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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/note="HYPOTHETICAL 103.9 KDA PROTEIN homolog [Homosapiens] (SPTR|AAL55781, evidence: FASTY, 85.5%ID, 97.4%length, match=2763)"
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Please visit our web site for further details.
URL:http://gancome.gsc.riken.jp/
URL:http://fancom.gsc.riken.jp/.
Location/Qualifiers
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/srrain="C57BL/GJ"
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/db_xref="raxon:I0090"
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Neuherberg, GERNANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BWEZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp434C0829) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin,
Please contact RZPD for ordering:
http://www.rzbd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434C0829
http://www.rzbd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434C0829
Further information about the clone and the sequencing project is
available at http://mips.gf.de/projects/cdna/.
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Rochrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
                                  2538 AGTGAAGCCTGACCCAGGAAAAGCAACCTAGTGGAGATCATGGATGTGAACGTCAG
                                                                                                    lleuAspSerAspIleLysValGlnLysIleArgAlaHisSerAspLeuSerThrValIl
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               uValGlnProAspProArgLysSerGlyLeuValGluLeuThrLeuGlnValGlyValGl
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                                                 GCCAACCATCTACCATCATGATGGCAGCCAGAGCACGGATGACGATAAAATTGTCCA
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                                                                 GlnSerSerAspAspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySerGlu
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KLSKLVPGNYTFSLITVVDSDGATNSTTANLITVNKAVDYPPVANAGPNQVITLPQNSIT
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                Vector pSportl;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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N-terminus truncated"
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GlySerAla---GluTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPhe--- 195
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Matches:
Conservative:
Mismatches:
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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This sequence was made by sequencing genomic exons and ordering
                                                                 ||| |||||||||||||:: :::::: |||||| arcattgtgcaaaaatggtatttttgtt
                                                                                                         ArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysValLeuArgValAspThrAla
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| AAAAGCAAGTACAAGATCCTGGATGCCACGGAT---CAGGAAAGCCTGGAGCTGAAAGCCAA
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                                              GlnSerArgProPheLysValLeuLysAlaAlaGluValAlaArgAsnLeuHisMet
                                                                                                                                                                     GlyCysLeuLeuLysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCysIle
                                                                                                                                                                                                                                  CysSerHisLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSerAsn
                                                                                                                                                                                                                                                                                             CysGluTrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThrGly
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
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          Direct Submission Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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HTC 03-APR-2004

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Adachi, J. Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Haramato, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatun, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kauka, M., Kojima, Y., Kolma, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamara, M., Nishi, K., Nomura, K., Numaza, K., Numaza, M., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sagaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Sogabe, Y., Tangami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Tayamishi, A., Muramatsu, M. and Hayashizaki, Y.
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Analysis of the mouse transcriptome based on functional annotation 6.60,770 (ull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2189)
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Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    he FANTOM Consortium and the RIKEN Genome Exploration Research
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Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                               Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 9279253
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                                                                                                                                                                       Chordata;
                                                                                        Mus musculus (house mouse)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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407 lThrValSerSerGluAsnAlaPheGlyGluGlyPheValAsnValThrVally8ProAl 427
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LeuGluGluMetSerGluTyr***AspAspTyrArgGluLeuGluLysAspLeuLeuGln
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                                                                                                                                                                                                                                          HisTyr------LeuAsnGlu-SerAlaSerThrProAlaProLysLeuProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 aAlaProSerGluSer----ThrProSer---GluLeuProIleSerProThrThrAl
                                                                                                                     GlyserAla---GluTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPhe-
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                                                          Proser---GlyLysGlnGluPro-
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                                                                                                                                                   mouse cDNA library'
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                                                                                                                                                                                 138. ... >2189
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PROTEIN homolog [Homo sapiens] (SPTR|AALS5781, evidence:
FASTY, 85.5%ID, 97.4%length, match=2763)
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Matches:
Conservative:
Mismatches:
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URL:http://fantom.gsc.riken.jp/
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Research Institute, cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, Helix Research Institute.
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                                                                      /organism="Homo sapiens"
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/db xref="taxon:9606"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 842)
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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Contact: Takao Isogai
Genomics Laboratory
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKPZ); Email s.wiemann@dkfz- heidelberg-de; sequenced by BMFZ (Blomedical Research Center at the Charite, sequenced by BMFZ (Blomedical Research Center at the Charite.) Berlin/Germany) within the cDNA sequencing consortium of the German
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1 (Dases 1 to 597)
1 (Acahrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)
Unpublished (1999)
                                                                                   TyrThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThrAla***ValThr
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This is the 5' sequence of the clone insert
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/lab hose="NHIOB (TI phage resistant)"
/clone lib="NHI BMAP_GHO"
/note="Organ: Brain; Vector: pYX- Asc; Site 1: BCOR I;
/note="Organ: Brain; Vector: pYX- Asc; Site 1: BCOR I;
/note="Organ: Brain; Vector: pYX- Asc; Site 1: BCOR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soarse, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel: First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with BCOR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Montal Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ramanla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. (Abases 1 to 710)

NIH-MGC http://mgc.nci.nih.gov/.

Longublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at thtp://genome.uiowa.edu/distribution/mousefi.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                          CB722905 710 bp mRNA linear EST 09-JUL-2003 UI-M-GHO-cef-i-19-0-UI.rl NIH BMAP_GHO Mus musculus cDNA clone IMAGE:6838844 5', mRNA sequence.
                      LeuSerAlaMetGlnGluGlyAspTyrThrPheGln-LeuLysValThrAsp-SerSerA 606
                                                                              606 rgGlnGlnSerThrAla-**ValThr-ValIleValGlnProGluAsnAsn 622
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Mus musculus"
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/strain="C57BL/6"
/db.xref="Lexon:10090"
/clone="INAGE:6838844"
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Location/Qualifiers
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Mus musculus
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CB722905.1 GI:29780047
EST.
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TITLE
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COMMENT
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ACCESSION
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AUTHORS
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BP229849 Sugano cDNA library, fetal brain Homo sapiens cDNA clone FBR04757, mRNA sequence.
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Genome Project.

No s1 sequence available.

No s1 sequence available.

This clone (DKPZp43400729) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                                1..597

| Organism="Homo sapiens"
| Mol Lype="MRNA"
| Mb Xres="texon: 9606"
| Clone="DKEZp43400729"
| Lissue_type="testis"
| dev_stage="adult"
| Abb_host="BH108"
| Clone lib="434 (synonym: htes3)"
| /note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
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                                                                                                                                                                                                                                                                                                                              AspSerAspGlyAlaThrAsnSerThrThrAlaAlaLeuIleValAsnAsnAlaValAsp
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Matches:
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Mismatches:
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98.99%
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Best Local Similarity:
Query Match:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 599)

2 Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizuhima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukishms.u-tokyo.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 GAACTGAGGCCCAAATATGGTATCAAGCACCGAAGCACAGAGCACAACTCCAGCCTGATG
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/mol_type="mRNA"
/clone="FBR04757"
/tisque_type="brain"
/dew stage="fetal"
/clone_lib="Sugano cDNA library, fetal brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           598
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                                               Homo sapiens (human)
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1 (bases 1 to 842)

2S Smith, T.P.L.; Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.

Porcine EST collection using a normalized library constructed from embryos representing early developmental stages

(contact: Smith TPL

(mpublished (2003)

Contact: Smith TPL

(DSA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4366

Fax: 402 762 4366

Fax: 402 762 4366

Fax: 402 762 4366

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  ProProValAlaValValSerProGlnLeuGlnGluLeuThrLeuProLeuThrSerAla 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_trym="mRNA"
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/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: Not Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                      CK463785 842 bp mRNA linear 934714 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence. CK463785
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Sus scrofa
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LysHisValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMetGlnGlu 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                      302 GTGACTGTTATTGTGCAGCCTGAAATAACAAGCCTCCACAGGCAGATGCAGGCCCAGAT 243
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                                                                         533 AlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGlyAsnGln
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Search completed: October 12, 2005, 15:35:46 Job time : 6955 secs

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Adro0858 Human 254
Adg15055 Human 8EC
Adm36226 Murine SS
Adi21796 Novel hum
Aad11067 Human sec
Adf42453 Human SEC
Aah18563 Human SEC
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Aas6915 Human cDN
Aav89613 EST clone
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Abz77634 Nucleotid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 254P1D6B v.2 encoding cDNA SEQ ID NO:4.
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ADN47960_04
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/*tag= a
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                      ADM36226
ADI21796
AADI1067
ADF42453
AAH89908
ADG15051
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ACA25573
ABA21464
ADQ89963
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-MODBL=frame+_Dar.model -DEV=Xlp
-MODBL=frame+_Dar.model -DEV=Xlp
-MODBL=frame+_Dar.model -DEV=Xlp
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-LIST=45_-DOCALIGN=200_-THR_SCORE=pcr_-THR_MAX=100_-THR_MIN=0._ALIGN=15
-MODBE_LOCAL_-OUTFMT=pcr_-NORM=ext_-HEAPSIZE=500_-MINLEN=0_-NAXLEN=200000000
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-FGAPEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DELEXT=7_
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Adr00591 Human 254
Adr00860 Human 254
Adr00859 Human 254
Adr00595 Human 254
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(without alignments)
5428.540 Million cell updates/sec
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                                                                                                                                                                                                                                                    8780412
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                       nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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ADR00595
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Jakobovits A, Challita-Eid
   Kanner SB, Raitano AB, Ji
Perez-Villar JJ, Faris M;
(AGEN-) AGENSYS INC
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WPI; 2004-580991/56.

P-PSDB; ADR00594.

New 254P1D6B siRNA composition comprising a double si corresponds to the nucleic acid ORF sequence which es protein or corresponds to a subsequence of the ORF, i and treating cancer.

Claim 10; SEQ ID NO 4; 345pp; English.

The present invention describes a 254PlD6B small interfer composition that comprises a double stranded siRNA that the interfer acid open reading frame (ORF) sequence which the 254PlD6B protein, or corresponds to a subsequence of the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 consists essentially of, or consists of a peptide of eigenven contiguous amino acids of a protein of figure 2 (No.3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptic any of the 42 lists of peptides, given in the specificat that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or identical to an entire amino acid sequence of P1; (2) a that is a full complement of the polynucleotide describe generating a mammalian immune response directed to the generating, an a sample, the presence of a 254PlD6F-relate composition that status of a cell that expresses a protein of P1; (7) a per composition that comprises the composition described about those form; (8) an antibody or its fragment, which is a non-human transgenic animal that produces the antibody; (11) delivering a non-human transgenic animal that produces the antibody; (12) inhibiting growth, reproduction or survival of cance express the protein of P1: 254PlD6B has cytostatic active used in gene therapy. The compositions, molecules and me for treating and detecting cancer. The present sequence 254PlD6B v2, which is used in the exemplification of thromes

Sequence 6791 BP; 1812 A; 1542 C; 1684 G; 1753 T; 0

		20	571	40	631	9	691	80	751
6791 1069 3 0 0		MetalaproproThrGlyValLeuSerSerLeuLeuLeuLeuValThrIleAlaGlyCys	AFGGCGCCCCCCACAGGTGTCTCTTCATTGCTGCTGCTGGTGATTGCTGGTGTTGT	AlaArgLysGlnCysSerGluGlyArgThrTyrSerAsnAlaVallleSerProAsnLeu	GCCCGTAAGCAGTGCGAGGGGGGGGACATATTCCAATGCAGTCATTTCACCTAACTTG	GluThrThrArg11eMetArgValSerHisThrPheProValValAspCysThrAlaAla	GAAACCACCAGAATCATGCGGGTGTCTCACCTTCCCTGTCGTAGACTGCACGGCCGCT	CysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuVal	TGCTGTGACCTGTCTGTGTGTTGTTGTTTCGAGGCCGCTGCTGGTG
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res: arity: milarity:	-3 (1-107								
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	10-764-390	<b>H</b>	512	21	572	41	632	61	692
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id PM, Ge W;	<b>3</b> 8	752 AGCTGCCCCACAAAGAGAACTGTGAGCCCAAGAAGATGGGCCCCATCAGGTCTTATCTC 811
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stranded siRNA that encodes the 254PlD6B useful for detecting	දි සි	121 LeudsnargGlySerProSerGly1leTrpGlyaspSerProGludspIleArgLysAsp 140
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r 25 contiguous sition that comprises,	à	
of eight, nine, ten, or re 2 (P1, see SEQ ID	ପ୍ଧ	1052 GAGTACACGGACTGGGGCCTACTGCCGGGCGGCCGTCCATCTGTTGGA 1111
lfication, or a protein 3, or 99% homologous or	ò	AspSerProAlaValProAlaGluThrGlnGlnAspProGluLeuHisTyrLeuAsnGlu
(2) a polynucleotide sing a polynucleotide	q	1112 GACAGTCCTGCGGTGCCAGCGGAGACGCAGCAGCACCTGAGCTCCATTACCTGAATGAG 1171
scribed above; (4) the protein of P1; (5) related protein or a	δλ O	221 SerAlaSerThrProAlaProLysLeuProGluArgSerValLeuLeuProLeuProThr 240
that modulates the 7) a pharmaceutical ed above in a human	ò	241 ThrProSerSerGlyGluValLeuGluLysGluLysAlaSerGlnLeuGlnGluGlnSer 260
nich is monoclonal; (9)	ନ୍ଧ (	
ing a cytotoxic agent protein of P1; and f cancer cells that	රු සි	261 SSTRBIBSERSTGILYVALDERMETPROSTRIBSERTBURYCOFALBSELDE Z80 1292 AGCAACAGCTCTGGAAAAGGGTTCTAATGCCTTCCCATAGTCTTCCTCCGGCAAGCCTG 1351
activity, and can be and methods are useful Lence encodes the human	λŏ	GluLeuSerSerValThrValGluLysSerProValLeuThrValThrProGlySerThr
of the present nromosome 6p22.	q <sub>Q</sub>	
0 U; 0 Other;	y da	301 GluHisSerIleProThrProProThrSerAlaAlaProSerGluSerThrProSerGlu 320
791 069	δό da	321 LeuprolleSerProThrThrAlaProArgThrValLysGluLeuThrValSerAlaGly 340
	ò	341 AspAsnLeulleIleThrLeuProAspAsnGluValGluLeuLysAlaPheValAlaPro 360
	q <sub>C</sub>	1532 GATAACCTAATTATAACTTTACCCGACAATGAAGTTGAACTTGAAGGCCTTTGTTGCGCCA 1591
	δ δ	361 AlabrobrovalgluthrthryvasnTyrglutrpasnLeullesserHisProThrasp 380
	ò	381 TyrGlnGlyGlulleLyeGlnGlyHisLysGlnThrLeuAsnLeuSerGlnLeuSerVal 400
aValileSerProAsnLeu 40	අු	1652 TACCAAGGTGAAATAAAACAAGGACACAAGCAAACTCTTAACCTCTCTCAATTGTCCGTC 1711
	P O	401 GlyLeuTyrValPheLygValThrValSerSerGluAgnAlaPheGlyGluGlyPheVal 420
	ð	421 AsnyalThrValLysProAlaArgArgValAsnLeuProProValAlalSerPro 440
uG1yArgCy81YrLeuval 80 	අු	1772 AATGTCACTGTTAAGCCTGCCAGAAGAGTCAACCTGCCACTGTGTGTTTTTTCCCC 1831
	که ا	441 GlnLeuGlnGluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThr 460

2912 ACAGACACTGCCACTGGGAAGTGCAGCCAGACCCTAGGAAGAGTGGCCTGGTGAGGCTG 2971  821 Thrieudlivalidy and the state of t	ADRO0591 the ADRO0591 standard; CDNA; 6791 BP.  XX AC ADRO0591; XX DT 04-NOV-2004 (first entry) XX DE Human 254PlD6B v.l clone LCP-3 encoding CDNA SEQ ID NO:2. XX XX XX XX X4 254PlD6B, small interfering RNA; siRNA; immune response; XX XX X4 254PlD6B v.l clone LCP-3; gene therapy; cancer; human; XX XX XX XX XX XX XX XX XX XX XX XX XX
1832 CAACTGCAAGAGCTCACTTTGCCTTTGACGTCAGCCCTCATTGATGGCAGCACCAAGTACA 1891   461   45p4sgPhhcflullevalsestryl	721 AlaArgaladlyGlyArgHisValLeuValLeuPcAshAsnSerIleThrLeuAspGly 740  2672 GCCGGGCTGGTGGTTCTTGTGCTTCCCATAATTCCATTACTTTGGATGGT 2731  2672 GCCGGGCTGGTGGCATGTTCTTGTGCTTCCATAATTCCATTACTTTGGATGGT 2731  741 SETATGSETTHTASpAspGllArgIIEValSerTyCLeuTrplleArgAspGlyGlnSer 760  1

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254P1D6B protein, or corresponds to a subsequence of the ORF, where the 254P1D6B protein, or corresponds to a subsequence of the ORF, where the consists essentially of or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (PL, see SEQ ID NO.3, 5 or 7 ADRO0592, ADRO0594 or ADRO0596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein CC that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98 homologous or identical to an entire amino acid sequence of P1; (2) a polynuclectide that is a full complement of the polynuclectide described above; (4) centar in a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related polynuclectide; (6) a composition that modulates the captured or in a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related polynuclectide; (6) a composition that modulates the captuid or in a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related protein of P1; (7) a pharmacentical composition that comprises the composition described above in a human control or an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and correct cells that composition or survival of cancer cells that expresses the protein of P1; and cused in a number of partine and described are used in a number or an order of a correct cells and each the protein of P1. 254P1D6B has cytostatic activity, and can be corrected to the protein of P1. 254P1D6B has cytostatic activity, and can be corrected to the protein of P1. 254P1D6B has cytostatic activity, and can be protein or aurainal agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating and detecting caneer. The present sequence encodes the human 254PID6B v.1 clone LCP-3, which is used in the exemplification of the present invention. The human 254PID6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                   Jakobovits A, Challita-Eid PM,
                          /transl_except= (pos:935. .937,aa:Xaa)
/transl_except= (pos:980. .982,aa:Xaa)
/transl_except= (pos:2345. .2347,aa:Xaa)
/note= "Xaa is any amino acid"
product= "254P1D6B v.1 clone LCP-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; SEQ ID NO 2; 345pp; English.
                                                                                                                                                                                                                                                               23-JAN-2004; 2004WO-US001965
                                                                                                                                                                                                                                                                                                               24-JAN-2003; 2003US-0442526P
                                                                                                                                                                                                                                                                                                                                                                                                                                                Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                                                                                                                                                                     Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004-580991/56.
                                                                                                                                                                                                                                                                                                                                                                  (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ADR00592.
                                                                                                                                                           WO2004067716-A2
                                                                                                                                                                                                            12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                        SB,
                                                                                                                                                                                                                                                                                                                                                                                                                     Kanner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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Sequence 6791 BP; 1809 A; 1537 C; 1677 G; 1751 T; 0 U; 17 Other;

Alignment Scores:

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6791
1071
0
1
0
0
Length:
Matches:
Conservative:
Mismatches:
                                                             US-10-764-390-3 (1-1072) x ADR00591 (1-6791)
         5574.00
99.91%
99.91%
99.89%
                            Similarity:
                   Percent Similarity:
                                    Query Match:
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20 MetAlaProProThrGlyValLeuSerSerLeuLeuLeuValThr1leAlaGlyCys

1471 1111 AGCAACAGCTCTGGAAAAGAGGTTCTAATGCCTTCCCATAGTCTTCCTCCGGCAAGCCTG 1351 GAGCTCAGCTCAGCTCACCGTGGAAAAGCCCCAGTGCTCACAGTCACCCCGGGGGTACA 1411 1051 260 AlaProProValGluThrTyrAsnTyrGluTrpAsnLeuIleSerHisProThrAsp 380 300 100 871 140 240 280 691 751 811 120 160 991 180 200 631 571 9 80 40 GluHisSerIleProThrProProThrSerAlaAlaProSerGluSerThrProSerGlu GAGCACAGCATCCCAACACCTCCCACTAGCGCAGCCCCCTCTGAGTCCACCCCATCTGAG LeuProlleSerProThrThrAlaProArgThrValLysGluLeuThrValSerAlaGly AspAsnLeuIleIleThrLeuProAspAsnGluValGluLeuLysAlaPheValAlaPro GluLeuSerSerValThrValGluLysSerProValLeuThrValThrProGlySerThr LeudandrgGlySerProSerGlyIleTrpGlyAspSerProGludapIleArgLysAsp Leu\*\*\*PheLeuGlyLysAspTrpGlyLeuGluGluMetSerGluTyr\*\*\*AspAspTyr 161 ArgGluLeuGluLysAspLeuLeuGlnProSerGlyLysGlnGluProArgGlySerAla 992 CGGGAGCTGGAGAAGGACCTCTTGCAACCCAGTGGCAAGCAGGAGCCCAGAGGGGAGTGCC 1052 GAGTACACGGACTGGGGGCCTACTGCCGGGCAGCGAGGGGGCCTTCAACTCCTCTGTTGGA ThrProSerSerGlyGluValLeuGluLysGluLysAlaSerGlnLeuGlnGluGlnSer SerAsnSerSerGlyLysGluValLeuMetProSerHisSerLeuProProAlaSerLeu 512 ATGGCGCCCCCCACAGGTGTGCTCTTTTCATTGCTGCTGGTGACAATTGCAGGTTGT SerCysProHisLysGluAsnCysGluProLysLysMetGlyProIleArgSerTyrLeu AGCTGCCCCCACAAGAGAACTGTGAGCCCAAGAAGATGGGCCCCCATCAGGTCTTATCTC ThrPheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMet 932 TIGMCCTITCTAGGCAAAGATIGGGGCCTAGAGGAGAIGTCTGAGTACKCAGAIGACTAC GluTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsnSerSerValGly AspSerProAlaValProAlaGluThrGlnGlnAspProGluLeuHisTyrLeuAsnGlu SeralaSerThrProAlaProLysLeuProGluArgSerValLeuLeuProLhr 21 AlaArgLysGlnCysSerGluGlyArgThrTyrSerAsnAlaValIleSerProAsnLeu 572 GCCCGTAAGCAGTGCAGCGAGGAGGACATATTCCAATGCAGTCATTTCACCTAACTTG GluThrThrArg11eMetArgValSerHisThrPheProValValAspCysThrAlaAla CysCysAspLeuSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuVal 872 221 1172 1232 1292 1352 1412 361 241 261 281 301 321 341 752 812 121 141 181 201 101 41 61 692 81 셤 셤 g ò g ð 셤 ઠ 셤 ò d ર્જ g જે 셤 ઠે 셤 ò g 8 셤 ð g ଚ g 셤 q ò 8 ઠે g ð ર્જ 6

741 SerArgSerThrAspAspGlnArg1leValSerTyrLeuTrp11eArgAspGlyGlnSer 760 [	30 30 31 31	881 LysAlaAlaGluValAlaArgAsnLeHiisMetArgLeuSerIysGluLysAlaAspPhe 900 3152 AaAGCTGCTGAAGTGCCCGAAATCTGCACATCCGGCTCTCAAGGGAGGCTCACTTC 3211 901 LeuLeuPheLysValLeuArgValAspThrAlaGlyCysLeuLeuLysCysSerGlyHis 920 11	941 IleGlnArgTyrIleTrpAspGlyGluSerAsnCysGluTrpSerIlePheTyrValThr 960 3332 ATACAGCGTTATATCTGGGAGGAGGACTGGATGGATGGAT	1001 MetAspGluGlnGluArgMetGluLeuArgProLysTyrGlyIleLysHisArgSerThr 1020 3512 ATGGATGAACAGGAAAGAACTGAGGCCCAAATATGGTATCAAGCACCGAAGCACCA 3571 1021 GluHisAsnSerSerLeuMetValSerGluSerGluBheAspSerAspGlnAspThrIle 1040	1051 ABIGINATION
86868686	8 6 8 6 8 6	8 6 8 6 8 6	8 6 8 6 8	\$ 8 \$ 8 \$	SUL
400 1711 420 1771 1831 460	1891 480 1951 500 2011 2071	540 2131 560 2191 580	600 2311 620 2371,	2431 660 2491 680 2551	700 2611 720 2671 740
381 TyrGlnGlyGlulleLysGlnGlyHisLysGlnThrLeuAsnLeuSerGlnLeuSerVal 40  1652 TACCAAGGTGAAATAAAACAAGGACACAAGCAAACTCTTAACCTCTCTCAATTGTCCGTC 17  401 GlyLeuTyrValPheLysValThrValSerSerGluAsnAlaPheGlyGluGlyPheVal 42  1712 GGACTTTATGTCTTCAAAGTCACTGTTTCTAGTGAAAACGCCTTTGGAGAAAGGATTTGTC 17  421 AsnValThrValLysProAlaArgArgValAsnLeuProProValAlaValValSerPro 44  1772 AATGTCACTGTTAAGCCTGCAGAAGAGTCAACCTGCCACCTTGGAGAGTTTTCTCC 18  441 GlnLeuGlnGluGluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThr 46  441 GlnLeuGlnGluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThr 46  1913 CAAATGCAAAACTCTAATTCTA		ValAsnAsnAlaValAspTyrProProValAlaAsnAlaGlyProAsnHisThrIleThr 54  GTGAACAATGCTGTGGACTACCCACGGTTGCTAATGCAGGACCAATCACACCCATAACT 21.  LeuProGlnAsnSerIleThrLeuAsnGlyAsnGlnSerSerAspAspHisGlnIleVal 56  TTGCCCCAAAACTCTTTGAATGGAACCAGGTGACGACGACCAGATTGTC  LeuTyGCTCAAAACTCTTTGAATGGAACCAGACGACGACGACGACGACTGTC  LeuTyGluTrpSerLeuGlyProGlySerGluGlyLysHisValValMetGlnGlyVal 58  LeuTyGGATTGCCTGGAGTGACGAGGACACACGCAGATTGTC  LeuTyGAGTGCTCCTGGAGTGACGAGGAGAGACACACGCGCACACACA			ValThrGlyLeuglnValGlyThrTyrHisPheArgLeuThrValLyBAspGlnGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG

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The present interaction describes a 237100 small interactions are present interaction that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the Catalloss protein, or corresponds to subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 23, 24, or 25 contiguous consists assentially of or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a pertide of eight, nine, ten, or eleven contiguous amino acids of a pertide of eight, nine, ten, or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) centraling, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related polynucleotide (6) a composition that modulates the composition that modulates the composition that modulates the composition that modulates the composition described above; (6) an arrival or a protein of F1; (7) a pharmaceutical control or a perting that composition described above in a human and that composition that modulates the composition that modulates the composition that composition that modulates the composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that composition that modulates the composition that modulates the composition that modulates the compositio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New 254PlD6B BiRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a 254P1D6B small interfering RNA (siRNA)
                                                                                                                                                                               254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.3; chromosome 6; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jakobovits A, Challita-Eid PM,
                                                                                                                                                     254PlD6B; small interfering RNA; siRNA; immune response;
                                                                                      Human 254P1D6B v.3 nucleotide sequence SEQ ID NO:271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; SEQ ID NO 271; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN-2004; 2004WO-US001965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JAN-2003; 2003US-0442526P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kanner SB, Raitano AB, J
Perez-Villar JJ, Faris M;
                               04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-580991/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                     WO2004067716-A2
                                                                                                                                                                                                                                                                           Homo sapiens.
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SO	Sequence 6797 BP; 1812 A; 1542 C; 1686 G; 1757 T; 0 U; 0 Other;	6797	BP;	1812	Ä,	1542	Ċ;	1686	Ü	1757	Ŧ,	0	::	ŏ	her;	
Alig	Alignment Scores:	res:														
Pred	Pred. No.:			0				Length:	ä		w	797	_			
Score:	 •			554	5546.50	_		Matches:	es:		-	1069	_			
Perc	Percent Similarity:	arity	••	99.53%	33%			Conse	r.	Conservative:	0	_				
Best	Local Sin	nilar	ity:	99	53%			Mismatches:	tch	e8:	•	_				
Quer	Query Match:		ı	66	408			Indels			(4					
DB:	i			13				Gaps:			_					

Oy 1 Metalal Db 514 ATGGCG Oy 19 YCY8A1 Db 574 TTGTI  Db 574 TTGGA OY 39 ILEUGI OY 59 AAIACY OY 79 UVAISE Db 754 GGTGAG OY 99 TLEUTH Db 754 GGTGAG OY 119 TMETLE OY 1139 SASDLE Db 934 GGACTT OY 179 TAIAGI Db 994 CTACCG OY 179 TAIAGI Db 1054 TGCCCC	MetalaproProThrdlyValLeuSerSerLeuLeuLeuValThrIleAlaG1 19
	GCCCCCCAGGGTGTGCTCTTCATTGCTGCTGGTGACAATTGCTTTGG 573  1aArgLysGlnCysSerGluGlyArgThrTyrSerAshlaVall1eSerProAs 39  1ccGTAAGGAGGAGGAGGAGAATTCCAATGCTGTCATTTCACCTAA 633  1uThrThrArgleMetArgVBSerHisThrPheProValValAspCysThrAl 59  1uThrThrArgleMetArgAGGAGGACATATTCCACGTCATTTCACCTAA 633  AAACCACCAGAATCATGCGGGGTGTCTCACACCTTCCCTGTCGTAGACTGCACGGC 693
	CCCGTAAGCAGTGCAGCGAGGACATATTCCAATGCAGTCATTTCACCTAA 633 luthrthrakgtaleMetArgValSerHisThrPheProValValAspCysThrAl 59 luthrthrakgtaleMetArgValSerHisThrPheProValValAspCysThrAl 59 AAACCACCAGAATCATGCGGGTGTCTCACACCTTCCCTGTGGTAGACTGCACGGC 693
	UThrThrargIleMetargValSerHisThrPheProValValAspCysThral 59 
	AAACCACCAGAATCATGCGGGTGTCTCACACCTTCCCTGTCGTAGACTGCACGGC 693
	ysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLe 79
	<u> éctereacciercaecteraccideccidectegragiticaaggecegeracet 753</u>
	erCysProHisLysGluAsnCysGluProLysLysMetGlyProlleArgSerTy 99
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	hrpheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMe 119
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	euksnargGlySerProSerGlyIleTrpGlyAspSerProGluAspIleArgly 139
	rgaacagggcrccccrcggggarcrgggggacrcaccrgaggararcagaaa 933
	eu***PheLeuGlyLysAspTrpGlyLeuGluGluMetSerGluTyr***AspAs 159
	TGCCCTTTCTAGGCAAAGATTGGGGCCTAGAGGAGATGTCTGAGTACTCAGATGA 993
	rgGluLeuGluLysAspLeuLeuGlnProSerGlyLysGlnGluProArgGlySe 179
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	llufyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsnSerSerVa 199
	AGTACAGGACTGGGGCTACTGCCGGCGAGGGGGGCCTTCAACTCCTCTGT 1113
Qy 199 1GlyAs	
Db 1114 TGGAGA	ccarraccrdaa 1
9n 6	aSerThrProAlaProLysLeuProGluArgSerValLeuLeuProLeuPr 
1	TTCAACCCCTGCCCCAAAACTCCTGAGAGAGTGTGTTGCTTCCCTTGCC
239 0	oSerSerGlyGluValLeuGluLysGluLysAlaSerGlnLeuGlnGluGl 2
	CAGGAACA
25.	ProAlaSe 2
129	CCGCCAAG
27	ProG1ySe
ù	CCGGGGAG
ō	ThrProSe
-À	ACCCCATC
2y 319 rGluLe	ValSerAl
ř	Ġrańceśc 15
Qy 339 aGlyAs	9 aGlyAspAsnLeuIleIleThrLeuProAspAsnGluValGluLeuLySAlaPheValAl 359

719 OArgalaArgalaGlyGlyArgHisValLeuValLeuProAsnAsnSerIleThrLeuAs 739 	pdlySerargSerThrAepaspdlnArglleValSerTyrLeuTrplleArgAepGlydl 75	759 nSerProAlaAlaGlyAspVallleAspGlySerAspHisSerValAlaLeuGlnLeuTh 779 	779 rAgnLeuValGluGlyValTyrThrPheHisLeuArgValThrAspSerGlnGlyAlaSe 799 	799 rAspThrAspThrAlaThrValGluValGlnProAspProArgLysSerGlyLeuValGl 819 	819 uLeuThrLeuGlnValGlyValGlyGlnLeuThrGluGlnArgLy8AgpThrLeuValAr 839 	839 gGlnLeuAlaValLeuLeuAsnValLeuAspSerAspIleLy8ValGlnLy8IleArgAl 859 	859 aHisSerAspLeuSerThrVallleValPheTyrValGlnSerArgProProPheLysVa 879 	879 lLeulysAlaAlaGluValAlaArgAsnLeuHisMetArgLeuSerLysGluLysAlaAs 899	899 pPheLeuLeuPheLysValLeuArgValAspThrAlaGlyCysLeuLeuLysCysSerGl 919 	919 yHisGlyHisCysAspProLeuThrLysArgCysIleCysSerHisLeuTrpMetGluAs 939 	939 nLeulleGlnArgfyrileTrpAspGlyGluSerAsnCysGluTrpSerllePheTyrVa 959 	959 IThrValLeuAlaPheThrLeuIleValLeuThrGlyGlyPheThrTrpLeuCysIleCy 979 	979 sCysCysLysArgGlnLysArgThrLysIleArgLysLysThrLysTyrThrIleLeuda 999 	999 pasnmetaspGluGlnGluArgMetGluLeuArgProLysTyrGlyIleLysHisArgSe 1019 	1019 rThrGluHisAsnSerSerLeuMetValSerGluSerGluPheAspSerAspGlnAspTh 1039 	1039 rIlePheSerArgGluLysMetGluArgGlyAanProLysValSerMetAanGlySerIl 1059 	1059 eArgAsnGlyalaSerPheSerTyrCysSerLysAspArg 1072 
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Conservative: Mismatches: Indels: fatches:

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The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to composition that comprises a double stranded siRNA that corresponds to subsequence of the encodes the 254PID6B protein, or corresponds to a subsequence of the composition where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of or consists of a peptide of eight, nine, ten, or cleven contiguous amino acids of a protein of figure 2 (Pl. see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00569), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein CC that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of Pl; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of Pl; (5) generating in a sample, the presence of a 254PID6B-related polynucleotide; (6) a composition that modulates the captum of a call that expresses a protein of Pl; (7) a pharmaceutical comprises the composition described above; (9) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and con-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and cytotatic activity, and can be useful in gene therapy. The composition or survival of cancer cells that express the protein of Pl; 254PID6B has cytostatic activity, and can be useful or the present invention. The human 254PID6B are useful or human 254PID6B are useful in very an expresse the protein of Pl; content sequence represents the protein and protein or the present inventio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
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254PID6B-related protein; cytostatic; gene therapy; cancer; human;
254PID6B v.1; chromosome 6; gene; ds.
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Perez-Villar JJ, Faris M;
ADR00859 standard; DNA; 6797 BP
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The present invention describes a 254PIDGB small interfering RNA (SiRNA) composition that comprises a double stranded siRNA that corresponds to composition that comprises a double stranded siRNA that corresponds to a subsequence which encodes the corresponds to a subsequence of the oncodes the corresponds to a subsequence of the offer, where the couples stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID CO NO:3, 5 or 7 ADR00529, ADR00594 or ADR005956), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein control that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) generating a mammalian immune response directed to the protein of proceed that is a full complement of the polymucleotide described above; (4) composition that modulates the composition that modulates the composition that comprises the composition that modulates the composition that comprises the composition that modulates the composition that produces the antibody or its fragment, which is monoclonal; (2) a non-human transgenic animal that expresses the antibody; (10) a non-human transgenic animal that expresses the protein of P1; and correct or a diagnostic agent to a cell that expresses the protein of correct correct correct coll that expresses the protein of correct correct correct correct coll that expresses the protein of correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct correct corre
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eArgAsnGlyAlaSerPheSerTyrCysSerLysAspArg 1072
                       3694 CAGAAATGGAGCTTCCTTCAGTTATTGCTCAAAGGACAGA 3733
                                                                                                                                                                                                                                                                           Human 254P1D6B v.3 encoding cDNA SEQ ID NO:6
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739. .3930
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                                                                                                                                     ADR00595 standard; cDNA; 6991
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             used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence enrodes the human 2541D6B v.3, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                     681 TTATGGTGGATGCACTCATGGCAAAAAATCACTGGTGAGCATCATTTAAGAAGACCCAT 740
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express the protein of P1. 254P1D6B has cytostatic activity, and can be
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sGluLysalaSerGlnLeuGlnGluGlnSerSerAsnSerSerGlyLysGluValLeuMe 2	310 ralaalaproSerGluSerThrProSerGluLeuProlleSerProThrThrAlaProAr 330	TGAAGTTGAACTGAAGCCTTTGTTGCGCCACCTGTAGAAACAACTACTA 1 TGAAGTTGAACTGAAGCCTTTGTTGCGCCACGCGCCACCTGTAGAACAACTACTACTA 1 TGAAGTTGAATTGATTGTTGCGCCACGCGCCACCTGTAGAACAACTACTA 1 TGAATGGAATTTAATAAGCCACCCCACAGACTACCAAGGTGAAATAAAAAAAA	GCAAACTCTTAACCTCTCAATTGTCCGTGGACTTTATGTCTTCAAAGTCACTGTTTC 1  SERGIUASDTAPPGGTGGTGGACTTAATGTCTCTCAAAGTCACTGTTTC 1  ISERGIUASDTAPPGGTGTGTGTGAATTGTCAATGTCACTGTTAAGCCTGCCAGAAGAGT 2  IASDTCAAAACGCCTTTGGAGAAAGGATTTGTCAATGTCACTGTTAAGCCTGCCAGAAGAGT 2  IASDTCAAAACGCCTTTGGAGAAAGAATTGTCAATGTCACTGTTAAGCCTGCCAGAAGAGT 2  IASDTCAAAAACGCCTTTGGAGAAAGAATTGTCAATGTCACTGTTAAGCCTGCCAGAAGAGT 2	CAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAAGAGCTCACTTTGCCTTTGAC 206  **SerAlaLeulleAspGlySerGlnSerThrAspAspThrGlulleValSerTyrHisTr 470	490 gleuseraaniaakuseseccritoriasaasaasaasatricasritoreegretiade 1180 490 gleuseraanleuaspProGlyaanTyrserPheArgleuThrValThrAspSerAapGl 510 2181 CTTGTCTAACCTTGATCCTGGTAACTATAGTTTCAGGTTGACTGTTACAGACTCGGACGG 2240 510 yAlaThrAsnSerThrThrAlaAlaLeu1leValAsnAsnAshAspTyrProProProVa 530 5241 ACCCATAACTGTAACTGTAACTGTAACTGTAACACAACTAACAACTAACT	ASCCALIANTICIACANCIGEANCICITATION OF A STATE	2351 MANCCAGANGLAGTENCCAGATICSTCTCINIANSIGNICSTGGGGGG 2420 570 rGluGlyLysHisValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMe 590 [	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New 254P1D6B SIRNA composition comprising a double stranded SIRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human 254P1D6B v.3 transcript variant nucleotide sequence SEQ ID NO:269.
                                                                                                                                                                                                                      3621 AGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGGACAAAAAAGGACTAAAATCAG
                                                           gProLysTyrGlyIleLysHisArgSerThrGluHisAsnSerSerLeuMetValSerGl
                                                                                                                                                             uSerGluPheAspSerAspGlnAspThrIlePheSerArgGluLysMetGluArgGlyAs
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Perez-Villar JJ, Faris M;
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that is a full complement of the polynucleotide described above, (4) generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PiD6B-related polynucleotide, (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and can be used in gene therapy. The compositions, molecules and methods are useful captured the protein of P1. 254PiD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PiD6B v.3 transcript variant nucleotide sequence, which is used in the examplification of the present invention. The human 254PiD6B gene
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encodes the protein; (3) a composition comprising a polynucleotide
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Matches:
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Oy         550 yAsnGlnSerSerAspAspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySe         570           Db         2361 AAACCAGAGCAGTGACCATCACCAGATTGCCTCTATGAGTGGTCCTGGGTACCTGGGGGG         2420           Oy         570 rGluGlyLysHisValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMe         590           Db         2421 TGAGGCAAACATGTGTGTGTGAGAGGAGATACAGACGCCATACCTTCATTATCTGCAAT         2480           Oy         590 tGlnGluGlyAspTyrTrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerTh         610           Db         2481 GCAGGAAGGAGATATATACATTCAGCTGAAGGTGACAGATTCTTCAAGGCAACAGTCTAC         2540	Oy 610 rAla***ValThrValIleValGlnProGluAsnArgProProValAlaValAlaGl 630  2541 TGCTGTGGTGACTGTCATCCAGCCTGAAAACAATAGACCTCCAGTGGCCGG 2600  630 YProAspLysGluLeullePheProValGluSerAlaThrLeuAspGlySerSerSerSe 650  2601 CCCTGATAAAGAGCTGATCTTCCCAGTGGAAAGTGCTACCCTGGATGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	Oy 670 uMetGluAsnileAspLysAlaileAlaThrValThrGlyLeuGlnValGlyThrTyTHi 690	Oy 730   LeuproAsnAsnSerIleThrLeuAspGlySerArgSerThrAspAspGlnArgIleVa 750	Oy 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	QY         850 rAsp11eLysValGlnLysIleArgAlaHisSerAspLeuSerThrValIleValPheTY 870           DD         3261 GGACATTAAGGTCCAGAAGATTCGGGCCCACTCGGATCTCAGCACCGTGATTTTA 3320           QY         870 rValGlnSerArgProProPheLysValLeuLysAlaAlaGluValAlaArgAsnLeuHi 890           DD         3321 TGTACAGAGCCGCCTTTCAAGGTTCTCAAAGCTGCTGAAGTCGCCGAAATCTGCA 3380           QY         890 sMetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysValLeuArgValAspTh 910           DD         3381 CATGCGGCTCTCAAAGGCTGACTTCTTGCTTTTCAAGGTTTTTCAAGGTTGATAC 3440
CAGTGGCAAGCAGGCCCAGAGGAGTGCCGAGTACACGGACTACTGCCGGG 1280  yerGludlyAlaPheAenSerSerValGlyAspSerProAlaValProAlaGluThrGl 210	TGAGAGAGTGTGTTGCTTCCCTTGCCGACTACTCCTCTCAGGAGAGGTGTTGGAGAA	330 1700 350 370 370	GluTrpAsnleulleSerHisProThraspTyrGlnGlyGlulleLysGlnGlyHisLy  TGAATGAAATTTAATAAGCCCCCACAGACTACCAGGGGGAATTAAAAACAAA  TGAATGAATTTAATAAGCCACCCCACAGGTGAATTAAAAAAAA	Ashleuproprovalalavalyalserproglineuglingluleuthiceuproflection 450	510 510 5240 530 530 550

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  rAlaGlyCysLeuLeuLysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCy
                                             slleCysSerHisLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSe
                                                                                       rAsnCysGluTrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuTh
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2002US-0373824P.
2002US-0377883P.
2002US-0383218P.
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03-MAY-2002;
24-MAY-2002;
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GAPACCACCAGAATCATGGGGGTGTCTCACACCTTCCCTGTCGTAGACTGCAGGCCGCT

CysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuVal

GluThrThrArgIleMetArgValSerHisThrPheProValValAspCysThrAlaAla

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The invention relates to a novel isolated SECP (secreted protein)

Complepetide. The polypeptide of the invention demonstrates

Comeroprotective, relaxant, antithyroid, antidiabetic, cytostatic,

dermatological, immunosuppressive, antiinflammatory, thyromimetic,

antiallergic, cerebroprotective, gastrointestinal, hepatotropic,

continuities anticonvulsant, antiparkinsonian, antibacterial,

cantineumatic, cardiant, cardiovascular, anti-HIV and nootropic,

antiparasitic, fungicide, protozoacide, virucide, uropathic,

antirheumatic, cardiant, cardiovascular, anti-HIV and nootropic

contivities. The polypeptide may be useful in diagnosing, preventing and

treating disorders including neurodegenerative disorders such as

creating disorders including neurodegenerative disorders particularly

compotonic dystrophy and catatonia, endocrine disorders particularly

cdiabetes and Grave's disease, cancers such as leukaemia, cervical or

chreat cancer, immunological disorders including scleroderma, systemic

compotonic dystrophy and allergies, gastrointesfrial disorders

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compotonic dystroshy and allergies, gastrointes including atherosclerosis

compotonic dystroshy and allergies, gastrointes and hepatic diseases particularly cirrhosis. The polymuclectides may be

contranged to create humanised or transgence and hepatic diseases particularly cirrhosis. The polymuclectides may be

contranged to create
                                        Marquis JP, Lee SY, Elliott VS, Ramkumar J, Hafalia AJA;
Kable AE, Chawla NK, Emerling BM, Khare R, Jiang X, Jackson AA;
Hawkins PR, Jin P, Mason PW, Richardson TW, Swarnakar A, Lal PG;
Warren BA, Lee S, Griffin JA, Fu GK, Wilson AD, Xu Y, Bulloch SA;
Becha SD, Bhatia UG, Burrill JD, Blake JJ, Ho A, Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or infections.
Hafalia AJA;
--- X. Jackson AA;
Tal PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3808 BP; 1038 A; 921 C; 1006 G; 843 T; 0 U; 0 Other;
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ACCCTGCAGGTTGGTGGGCAGCTGACAGAGCAGCGGAAGGACACCCTTGTGAGGCAG 2586
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                                                                                                                                                                                                                                                                                                                                                      MetAspGluGlnGluArgMetGluLeuArgProLysTyrGlylleLysHisArgSerThr
                                                                                                                                                                                                                                                                                                                                                                                                GluHisAsnSerSerLeuMetValSerGluSerGluPheAspSerAspGlnAspThrIle
                                                                       LeuLeupheLysValleuArgValAspThrAlaGlyCysLeuLeuLysCysSerGlyHis
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                                                                                                                                                                                                  ------CAAAAAGGACTAAAATCAGGAAAAAAAGAAGTACACCATCCTGGATAAC
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                   LeuAlaValLeuLeuAsnValLeuAspSerAspIleLysValGlnLysIleArgAlaHis
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                                                                                                                          AAAGCTGCTGAAGTGGCCCGAAATCTGCACATGCGGCTCTCAAAGGAGGAAGGCTGACTTC
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This invention relates to novel membrane proteins that are associated with differentiation and/ or metabolic function of adipocytes, in particular of muse origin. Specifically, it refers to the isolated nucleic acid molecules encoding all or part of these proteins, appropriate antibodies and screening assays useful for the development of dry compositions derived thereof. The present invention describes these compositions as useful for the treatment of diseases associated with abnormalities of adipocyte function, such that they can be used to prevent, treat or disgnose obesity, hypertension, hyperlipaemia, diabetes and arteriosclerosis. Accordingly, they exhibit anorectic, antidiabetic, antiarteriosclerosis, antilipaemic and hypotensive activities.
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                                                                                                                                                                                            Mouse membrane and secretory proteins of adipocyte origin and polynucleotides encoding them for screening compounds as remedies for obesity, diabetes, arteriosclerosis, hypertension and hyperlipemia.
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(TAKE ) TAKEDA CHEM IND LTD
                                                        Funahashi T,
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P-PSDB; ADM36227.
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Best Local Similarity:
                                                        Matsuzawa Y,
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1440 CTCTGA 527 rProPr 1500 CCCTCC 547 rLeuAa					707 uThrVa 2040 TAATGT 727 sValle 2100 GGTGGT	747 nargll : : : :     2160 GGGGAT   767 eAspGl   2220 GAATCA	787 rPheHi 2280 GTTTCA 807 uValG1 2340 AGTGAA	827 yGlnLe 2400 TCAGCT 847 LLEUAB 2460 GCTGGA 867 eValPh ::::	2520 Grigin
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	AsnSerSerValGlyAspSerProAlaValProAlaGluthrGlnGlnAspProGluLeu :::       :::         :::	231 uArgSerValLeuLeuProLeuProThrThrProSerSerGlyGluValLeuGluLygGl 251 ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	271 oSerHisSerLeuProProAlaSerLeuGluLeuSerSerValThrValGluLysSerPr 291 786	311 aAlaProSerGluSerThrProSerGluLeuProlleSerProThrThrAl 328	UProAspAsnGluValGluLeuLysAlaPheValAlaProAlaProProValGluThrTh	387 nGlyHisLysGlnThrLeuAsnLeuSerGlnLeuSerValGlyLeuTyrValPheLysVa 407 :	aArgArgValAsnLeuProProValAlaValValSerProGlnLeuGlnGluLeuThrLe	TYTHISTEGIUGIUIIEASUGIYPTOPHEIIEGIUGIULYSTHYSETVAIASDSEYPT	
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1559 TTGGAAACCAGAGGCACGGATGACCACGGCATCACCAGCTATGAGTGGTCGCTCAG 1619 1679 ||-:::||||||| GCACAGATGACCAGAGAGTCGTCTCTTACCTTTGGGAGCAGAGTCGGGGACCTGA 1919 2039 2159 2339 2459 || |||||||:::||| ||| ||| |||||| |||||| ||||:: TCATTGTCAAAGAAGAAATAAACAAACCGCCAGTAGCCAAGATCGCTGGGAACGT 2099 ACGGGGCTACCAACTCCACCACTGCAAGCCTGACTGTGAACAAAGCTGTGGACTA 1499 567 587 687 707 767 867 647 erSerAspAspHisGlyIleValPheTyrHisTrpGluHisValArgGlyProSe 667 alAlaValLysLysGluAsnAsnSerProProArgAlaArgAlaGlyGlyArgHi 727 747 807 847 heTyrValGinSerArgProProPheLysValLeuLysAlaAlaGluValAlaAr 887 snGlyAsnGlnSerSerAspAspHisGlnIleValLeuTyrGluTrpSerLeuGl lyserGluGlyLysHisYalValMetGlnGlyValGlnThrProTyrLeuHisLe GCAGCAAAGGGAAGGTGGTGGTGGAGATGCAGGAGTTAGAACGCCAGCCCTGCAGCT alGluMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeuGlnValGl leValSerTyrLeuTrpIleArgAspGlyGlnSerProAlaAlaGlyAspValIl euThrGluGlnArgLysAspThrLeuValArgGlnLeuAlaValLeuLeuAsnVa SpSerAspIleLysValGlnLysIleArgAlaHisSerAspLeuSerThrValIl laGlyProAspLysGluLeuIlePheProValGluSerAlaThrLeuAspGlySe isLeuArgValThrAspSerGlnGlyAlaSerAspThrAspThrAlaThrValGl roValAlaAsnAlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIleTh

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gAsnLeuHisMetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysValLeuAr 907
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                                                                                                                                                                                                                                                                                                                                 2994 CCTGATGCATTCTGAATCGGAGCTGGACCACAC---GATGCCATCTTCACATGGCCAGA
           rlysArgCyslleCysSerHisLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAs
                                                                                                                                               eValLeuThrGlyGlyPheThrTrpLeuCysIleCysCysCysCysbysArgGlnLysArgTh
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13-SEP-2002; 2002US-00323739.
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The invention relates to an isolated polymucleotide encoding a polymeptide with biological activity. The polymucleotides and polymeptide with biological activity. The polymucleotides and identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polymucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising mathbodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents CDNA encoding a novel human protein.
                                                                                                                                                                                                                                                                           are
             New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGTACCTGTTTTATACTTGCTTTTGCTTCAGCGTTCTGTGGTTGTCAACAGATGCCAG 339
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181 uTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsnSerSerValGlyAs 201

Zhang J, Zhao QA, ou P, Drmanac RT,

Ren F, Zhang J G, Zhou P,

Tang YT, Asundi V, Goodrich RW, R Ghosh M, Xue AJ, Wehrman T, Weng Haley-Vicente D;

HYSE-) HYSEQ INC.

WPI; 2003-354603/33. P-PSDB; ADI21080.

1078   CAGAGAGCACTACCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCATACCCCATACCCATACCCATACCCATACCCATACCCATACCCATAC
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isteuseralametGlnGluGlyas 594 rgGlnGlnSerThrAla\*\*\*ValTh 614 alalavalalaglyProdspLysgl 634 1. yserserserspapaphisgl 654 CTGTGAATGTCATTGTCAAAGAAGA 2253 SpGlnArglleValSerTyrLeuTr 754 ||:::::: |TGTTAAATCACTCTGACCATCACCC 2433 alGluValGlnProAspProArgLy 814 alilevalPheTyrvalGlnSerAr 874
:::|||||||:::||||||||:: ATTACCCCCTGTGGCCAACGCAGG 1713 ||||||||| TCACCCTCTTTGGGAACCAGAGCAC 1773 || ||| ||| |||:::||||||| :TCAGCCCAAGCAGCAAAGGAAAGT 1833 ATGTGGTGATTACCCTACCCACGAG 2313 caecearecrcaagagreagcrece 2793 leThrLeuAsnGlyAsnGlnSerSe 554 euGlyProGlySerGluGlyLysHi 574 alGlyThrTyrHisPheArgLeuTh 694 hrLeuThrValAlaValLysLysGl 714 rgHisValLeuValLeuProAsnAs 734 alileAspGlySerAspHisSerVa 774 alGlyGlnLeuThrGluGlnArgLy 834 laArgAsnLeuHisMetArgLeuSe 894

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                                                                                                                                                                                                                                                                                                    1032 uPheAspSerAspGlnAspThrIlePheSerArgGluLysMetGluArgGlyAsnProLy 1052
                                                                                                                                                                                                                                                                                                                         3208 GCTGGACAGCGAT---GATGCCATCTTTACATGGCCAGACCGAGAGAGAGAGAACTCCT 3264
                                                                                                              2914 TTTTTGGATGGAGAATTTCATCAAGGTGCAGCTGAGGGATGGAGACAGCAACTGTGAGTG 2973
                                                                                                                                             974
          rLysGluLysAlaAspPheLeuLeuPheLysValLeuArgValAspThrAlaGlyCysLe 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; SECP; cell proliferative disorder; hepatitis; cirrhosis; autoimmune disorder; inflammatory disorder; acquired immune deficiency syndrome; AIDS; allergy; Grave's disease; anaemia; infection; cardiovascular disorder; myocardial infarction; congestive heart failure; angina pectoris; neurological disorder; Huntington's disease, Alzheimer's disease; Parkinson's disease; Cushing's syndrome; developmental disorder; stroke; gene therapy; renal tubular acidosis; transgenic animal; cancer; ss.
                                                                  sTyrThr1leLeuAspAsnMetAspGluGlnGluArgMetGluLeuArgPro-----Ly
                                                                                                                                                                                                                                 3148 AGCAGGCATCAAACAGAAAGGCCTTTTGCTAAGTAGCAGCCTGATGCACTCCGAGTCAGA
                                                 uLeuLysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCysIleCysSerHi
                                                                                         934 sLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSerAsnCysGluTr
                                                                                                                                   pSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThrGlyGlyPheTh
                                                                                                                                                                          rTrpLeuCy81leCy8Cy8Cy8Ly8ArgGlnLy8ArgThrLy81leArgLy8Ly8ThrLy
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/product= "Human SECP protein"
207. .353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein (SECP) cDNA #5.
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354. .3353
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10-JAN-2001; 2001WO-US000895

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The invention relates to human secreted proteins (SECP) and nucleic acid molecules encoding such proteins. SECP agonist and/or antagonist is useful for treating diseases associated with decreased expression or overexpression of functional SECP. The disorders treated include cell proliferative disorders such as cancer, arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, and psoriasis; autoimmune/ configuratory disorders such as acquired immune deficiency syndrome (ALDS), allergies, anaemia, asthma, autoimmune thyroiditis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, Grave's disease, continue, myocardial infarction, ischaemic heart disease and angina pertorial infarction, ischaemic heart disease and angina pectoris; neurological disorders such as stroke, Huntington's disease, contents, neurological disorders such as stroke, Huntington's disease, Alzheimer's disease, pick's disease, epilepsy, dementia, and parkinson's disease; and developmental disorders such as renal tubular acidosis and cushing's syndrome. SECP DNA is useful to create knock-in humanised animals (pigs) or transgenic animals (mice or rats) to model human charapy, to generate hybridisation probes useful in mapping the naturally concurring genomic sequence, and in molecular biological techniques. The
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                                                                                                                                                                                                                                                                     Au-Young J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human secreted protein useful for diagnosing, preventing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological and developmental disorders.
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Lu DAM, Yang J, Burford N, A
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Baughn MR,
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, 2000US-0177733P.
, 2000US-0178832P.
, 2000US-0179774P.
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P-PSDB; AAE05768.
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, Tang YT,
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Khan FA,
Reddy R;
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1370 CCATGGGGAAGGCTATGTGAACGTGAC  434 OVALALAVALVALSErPrOGINLEUGII  1430 CATTGCTATTGTGCACCTCAGTTCCAA  454 eASpGlySerGlnSerThrAspAspTh  1490 TGATGGTGAAGGCACTGATGATGAA  474 nGlyProPheIIeGluGluLysThrSe:  474 uAspProGlyAsnTytSerPheArgLee  494 uAspProGlyAsnTytSerPheArgLee  1550 GGGGCCTCTAAGAAGAAGAAGATTTC  494 UASpProGlyAsnTytSerPheArgLee  1610 CGTCCCTGGGAACTACACTTTCAGCTTT  514 rThrThrAlaAlaLeuIleValAsnAsi	1670 TACTACTGCAAACTGACAGTGAACAA 534 YPROABNHISTHRILETHILEUPROGI) 1730 CCCCAACCAAGTGATCACCCTGCCCCAA 554 TASPASPHISGINILEVALLEUTYGII 1790 TGATGATCATGCACCAGTGTATGAC 574 SVAlValMetGINGlyValGINTHPPR 574 SVAlValMetGINGLYVALGINTHPPR 1850 GGTGGAGATGCAGGTGTTAGAACACAGAACACAACACAACACAAACACAACACAAACACAAAACAAAA	594 ptyfinfnedineuliarsis	694 rVallygaspGlnGlnGlyLeuSerSe [
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	181 uTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsnSerSerValGlyAs 201   716   C	### SETSETGIVLYBGIUVALLEUWELPTOSETHISSETLEUPTOPT	1094 CCAGAĞCACCAGACCATACCCAĞTTATAAAĞĞA 1129 334 uLeuThrValSerAlaGlyAspAsnLeuIleIleThrLeuProAspAsnGluValGluLe 354 1130 ACTGGTGGTTGCTGGAGAGAGTGTCCAGATAACCCTGCCTAAGAATGAAGTTCAATT 1189 354 uLysAlaPheValAlaProAlaProProValGluThrTyrAsnTyrGluTrpAsnLe 374 1190 AAATGCATATCTCCCAGAACCACTAAAGAGAAACCTACCACCACGACTGGCAGCT 1249 374 ulleSerHisProThrAspTyrGlnGlyGluIleLysGlnGlyHisLysGlnThrLeuAs 394 1190 AAATGCATATGTTCTCCAGAACCACTAAAGAGAAAACTACCAGATCCTCAA 1309 374 ulleSerHisProThrAspTyrGlnGlyGluIleLysGlnGlyHisLysGlnThrLeuAs 394 1110 AAATGCATATCAACATGAGAAAAATGGAAAAATGCAGAAAATGC 1369 1310 ACTATCGAAGCTCACAGGCCTGTATGAATTCAAAATGC 1369 414 aPhGlyGluGlyPheValAsnValThrValLysProAlaArgAATGAAAATGC 1369 11 aPhGlyGluGlyPheValAsnValThrValLysProAlaArgAATAGAAAATGC 1369
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erValaspSerProValLeuArgLeuSerAsnLe 494 SINATAVATABPTYrProProVatAtaAsnAtaG1 534 | SepserSerArgGlnGlnSerThrAla\*\*\*valTh 614 hrLeuaspGlySerSerSersspaspHisGl 654 ladlyAspVallleAspGlySerAspHisSerVa 774 3luGlyValTyrThrPheHisLeuArgValThrAs 794 CAGTCAAGCCAGAGCCCCGTAAGAATCGGCCCCC 1429 |||| :: |TAACTGGGAATGTGGTGATTACCCTACCCACGAG 2329 ingluleuThrieuProleuThrSerAlaLeuil 454 luTrpSerLeuGlyProGlySerGluGlyLysHi 574 roTyrLeuHisLeuSerAlaMetGlnGluGlyAs 594 alArgGlyProSerAlaValGluMetGluAsnIl 674 erThrSerThrLeuThrValAlaValLysLysGl 714 laGlyGlyArgHisValLeuValLeuProAsnAs 734

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Percent Similarity:
Best Local Similarity:
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11-SEP-2002
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                                                                                                            |GlnLyg1|eArgAlaHisSerAspLeuSerThrVal1|eValPheTyrValGlnSerAr
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         pSerGlnGlyAlaSerAspThrAspThrAlaThrValGluValGlnProAspProArgLy
                  sSerGlyLeuValGluLeuThrLeuGlnValGlyValGlyGlnLeuThrGluGlnArgLy
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                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel human protein with cancer inhibiting function. Also disclosed is the polynucleotide encoding the protein, a method for preparing the polypeptide by a recombinant technique, and an antagonist against the polypeptide by a recombinant technique, and an treating diseases, such as cancers. The polypeptide is useful for treating diseases, such as cancers. The current sequence represents a human cancer inhibiting protein encoding CDNA.
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59.98%
47.71%
42.74%
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08-FEB-2001; 2001CN-00105311
                                                                                                         (SHAN-) SHANGHAI INST
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1671 TACTACTGCAAACCTGACAGTGAACAAAGCTGTGGATTACCCCCCTGTGGCCAACGCAGG 1730   534 yProAsnHisThrIleThrLeuProGlnAsnSrIleThrLeuAsnGlyAsnGlnSerSe 554	614 rValileValGlnProGluAsnAsnArgProProValAlaValAlaGlyProAspLygGl 634	2091 AATTATCTCATATCTCTGGGAAAAAACCAGGGACCTGATGGGGTCCGGGAATG 2150 674 leAspLysalaileAlaThrValThrGlyLeuGlnValGlyThrTyrHisPheArgleut 694 ::: :::::::		754 rpileArgAspGlyGlnGerProAlaAlaGlyAspValileAspGlySerAspHisSerV 774	
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C	### STACCAGIGGCTCTGCAGAGGTCCACAAGGGGATTACCAGTCCCCTAACCACAGA 914  277 OAlaSerLeuGluLeuSer	TGTCCCCCAGCCAGTGGCTCCCTACAGTTATGCTACCCCTACCCCCAGGCCTCTTT  rG1uSerThrProSerGluLeuProlleSerProThrThrAlaProArgThrValLysGl  ::	ACTGGTGGTATCTGCTGGAGAGAGTGTCCAGATAACCCTGCCTAAGATGAAGTTCAATT  ULYSALaPheValAlaProAlaProProValGluThrThrTyrAsnTyrGluTrpAsnLe	nleuserglnieuservalgivieuryrvalphelysvalthrvalsersergluasnal nleuserglnieuservalgivieuryrvalphelysvalthrvalsersergluasnal       ::   :::	434 OVALABAVALVALSERPROGINEGILLEUTRICEUPROGENTRESEATALGUII 454  [1:1]
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                                                                      erLysGluLysAlaAspPheLeuLeuPheLysValLeuArgValAspThrAlaGlyCysL
             934 isLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSerAsnCysGluT
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                                                 euleulysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCysIleCysSerH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                       3282 TGCATGGTCAGAATGGCTCTGTACCCAACGGG 3313
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2000US-00488725.
2000US-00552317.
2000US-0059442.
2000US-00534450.
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25-APR-2000;
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03-AUG-2000;
14-SEP-2000;
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130 TrpGlyAspSerProGluAspIleArgLysAspLeu***PheLeuGlyLysAspTrpGly 149
                                                                                                                                                                                                            The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemphilia), inhibition of tumour cell proliferation, suppression on inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the
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                                                                                                                            Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3918 BP; 1017 A; 1023 C; 1013 G; 865 T; 0 U; 0 Other;
     Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, M
ang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang
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ProserglyLysglnGluProArgGlySerAlaGluTyrThrAspTrpGlyLeuLeuPro 189

699 ---TCTTGGAGGCAGCCCACCCAGAGCTGCACTC---

LeuGluGluMetSerGluTyr\*\*\*AspAspTyrArgGluLeuGluLysAspLeuLeuGln

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881 ysAlaAlaGluValAlaArgAsnLeuHi	& 	1650 AGCTTGACTGTAGTAGACTCTGATGGAGCTACCAACTCTACTACTACTGGAAACCTGACAGTG 1709	යි
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2250 GCAAAGCCTGAGCTCTGTGAATGTCATT	: A 6	343 LeulleIleThrLeuProAspAsnGluValGluLeuLy8AlaPhe-ValAlaProAla-P 362 :::	& 8
2190 GACTGGGCTGCCAGTGGGGACCTATGTC	q &	323 IleSerProThrThrAlaProArgThrValLysGluLeuThrValSerAlaGlyAspAsn 342 :::	පි සි
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642 AlaThrLeuAspGlySerSerSerSerSer 	8 8	ThrGluHisSerIleBroThrPro	ò
622 ABINTGPTOVIOVAIALAVAIAGLYK    :::         2010 AATAAGCCTCCTCAGGCAGATGCAGGCC	à a	284SerValThrValGluLysSerProValLeuThrValThrProGlySer 299 	è 8
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522 AsnAsnAlavalAspTyrProProValA	₩ qq	190 GlySerGluGlyAlaPheAsnSerSerValGlyAspSerProAlaValProAlaGluThr 209          ::: 732	දු දු

AsnGlnSerSerAspAspHisGlnIleValLeu 561 isPheArgLeuThrVallysAspGlnGlnGlyLe 701 SerAspHisSerValAlaLeuGlnLeuThrAsnL 781 |||||||||| |rcrGacCatCatCcTatCTTTTTCTTTCAAACC 2489 TTTGTTCAAAACGAGCCTCCCCACCAGATCTTTA 2789 | Internated | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | Internation | I |:::|||||| || || ||||||||||::: CGINGIUGIYABDTYTHrPheGInLeuLysval 601 ProAsplysGluLeullePheProValGluSer 641 |||||||| |GATGATCAGAAATTATCTCATATCTCTGGGAA 2129 TIGICCAAGAACAATAAACAAACCAACCTATAGC 2309 CCTACCCACGAGGACATCAGAGCTGGATGGCTC 2369 ProAspBroArglysSerGlyLeuValGluLeuT 821 |||||||||||||||||:: |CCTGATCCCAGGAAAACAACCTGGTGGAGATCA 2609 741 661 841 GluGlyLysHisValValMetGlnGlyValGln 581 lavalLysLysGluAsnAsnSerProProArgAl 721 alSerTyrLeuTrpIleArg-AspGlyGlnSerP 761 TyrvalGlnSerArgProProPheLysValLeuL 881 uHisMetArgLeuSerLysGluLysAlaAspPheL 901 AspAspHisGlylleValPheTyrHisTrpGlu alLeuProAsnAsnSerIleThrLeuAspGlySe fhrGluGlnArgLysAspThrLeuValArgGlnL

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SerGlyLysGlnGluProArgGlySerAlaGluTyrThrAspTrpGlyLeuLeuProGly 190
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                                                                                                     2850 TGATATTCAAAGCCTTGGAAGTCAACACTGTCACATGTCAGCTGAACTGTTCCGACCATG
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                                                                         euLeuPheLysValleuArgValAspThrAlaGlyCysLeuLeuLysCysSerGlyHisG
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secreted protein; neuroprotective; relaxant; antithyroid;
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19-APR-2002; 2002US-0373824P.
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Length: Matches: Conservative: Mismatches:

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controlled to the polypeptide of the invention demonstrates protein)

polypeptide. The polypeptide of the invention demonstrates controlled to the polypeptide of the invention demonstrates controlled. Immunosuppressive, antidiabetic cytostatic, dermatological, immunosuppressive, antidiabetic cytostatic, carebroprotective, gastrointestinal, hepatotropic, anticonvulsant, antiparkinsonian, antibacterial, enpirotectic, fungicide, protozoacide, virucide, uropathic, antiparasitic, fungicide, protozoacide, virucide, uropathic, antiparasitic, cardiant, cardiava, anti-HIV and noctropic continuatic, cardiant, cardiava weeful in diagnosing, preventing and treating disorders including neurodegenerative disorders such as creating disorders including neurodegenerative disorders including corporate disorders including careconic dystrophy and catatonia, endocrine disorders particularly controlled disorders including scleroderma, systemic diabetes and Grave's disease, cancers such as leukaemia, cervical or breast cancer, immunological disorders including scleroderma, systemic culpuns erythematosus and allergies, gastrointestinal disorders e.g. Goodpasture's syndrome, infections particularly viral, bacterial, fungal, parasitic, cused to create humanised or transgenic animals, as well during gene to therapy procedures. The current sequence is that of the human SECP odna.
                                                                                                                                                                                                                                        Marquis JP, Lee SY, Elliott VS, Ramkumar J, Hafalia AJA;
Kable AB, Chawla NK, Emerling BM, Khare R, Jiang X, Jackson AA;
Hawkins PR, Jin P, Mason PM, Richardson TW, Swarmakar A, Lal PG;
Harren BA, Lee S, Griffin JA, Pu GK, Wilson AD, Xu Y, Bulloch SA;
Becha SD, Bhatia UG, Burrill JD, Blake JJ, Ho A, Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to a novel isolated SECP (secreted protein)
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24-MAY-2002; 2002US-0383218P
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AspProLeuThrLysArgCys1leCysSerHisLeuTrpMetGluAsnLeuIleGlnArg
                                                         caaaaa - - - ggaaaacccaagaggaaaagagaagracaagarccrggargccacggar - - -
                                                                                                                                                                                     GlnGluArgMetGluLeuArgPro----LysTyrGlyIleLysHisArgSerThrGlu
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                    944 TyrileTrpAspGlyGluSerAsnCysGluTrpSerIlePheTyrValThrValLeuAla
                                                                                        PheThrLeulleValLeuThrGlyGlyPheThrTrpLeuCysIleCysCysLysArg
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, Otsuki
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A, Nagai K
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27-ANG-1999; 99JP-00300253.
11-JAN-2200; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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Sugiyama T, Wakama
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The present invention describes primer sets for synchresising social in the present invention describes primer and an oligonucleotide complementary strand of a polyvucleotide which comprises one of the 5602 complementary strand of a polyvucleotide which comprises one of the 5602 uncleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polyvucleotide which comprises a 3'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 1'-end sequence, where the polynucleotide comprises a 1'-end sequence, where the complementary is a least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the capture of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as a saily without any specialised methods. AAH03166 to AAH03628 and AAH13633 to AAH0361842 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13622 represent invaries.
primer sets for synthesising 5602 full-
   present invention describes
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C; 711 G; 590 T; 0 U; 0 Other; Sequence 2796 BP; 763 A; 732

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                                                                                            LeuLysAlaPheValAlaProAlaProProValGluThrThrTyrAsnTyrGluTrpAsn 373
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TTAAATGCATATGTTCTCCAAGAACCACCTAAAGGAGAAACCTACCCTACGACTGGCAG
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        Length:
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Conservative:
Mismatches:
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GlyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGlyAsnGlnSer 553

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8; SEQ ID NO 18736; 2537pp + Sequence Listing; English

Claim

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1683 cagcidaacigirccgaccarggccacrargacrcgrrcaccaaacgcrgrarcrgagc 1742
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                   LeuLeuLysCysSerGlyHisGlyHisCysAspProLeuThrlysArgCysIleCysSer
                                                                                        934 HisLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSerAsnCysGlu
                                                                                                              974 ThrTrpLeuCyslleCysCysCysLysArgGlnLysArgThrLyslleArgLysLysThr
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98US-00036321
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This full-length cDNA clone, designated cw1233 3, codes for a novel human secreted protein (see AAW69430), i.e. cw1233 3 protein. It was isolated from a human foetal brain cDNA library using methods which are selective from a human foetal brain cDNA library using methods which are selective cor cDNAs encoding secreted proteins, or was identified as encoding a secreted protein on the basis of computer analysis of the encoding protein. Homology is shown to some database sequences. The invention provides isolated polymucleotides (see AAV58754-63) obtained from human adult testis, brain, retina or placenta, or from foetal kidney or brain cDNA libraries. These are all deposited as ATCC 98353. They canced novel human secreted proteins (see AAW65423-33) that may have e.g. nutritional activity, immune stimulating or suppressing activity, haemostatic activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, antiinflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition or other activities. They may also be used for diagnostic purposes ×88888888888888888888888

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; Sequence 52425, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; FAPPLICANT: Hyseq, Inc
TITLE OF INVERTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C1P3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2000-03-31
; PRIOR PILING DATE: 2000-03-31
; PRIOR PILING DATE: 2000-03-31
; PRIOR PILING DATE: 2000-03-31
; RIOR APPLICATION NUMBER: 09/649,167
; RIOR PILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO S-2425
; LENGTH: 19
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1.7%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels
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| NAME/KEY: misc_feature
| LOCATION: (1) ... (19)
| CTHER INFORMATION: Xaa = X or * as defined in Table 2
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                              Sequence 43, Application US/10764390

Publication No. US20040214212A1

GENERAL INFORMATION:

APPLICANT: Agensys, Inc.

APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

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APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

APPLICANT: Generalita-Eid, Pia M.

FILE REFERENCE: 51158-20081.00

CURRENT APPLICATION NUMBER: US60/442,526

PRIOR FILING DATE: 2004-01-23

PRIOR FILING DATE: 2004-01-23

PRIOR FILING DATE: 2004-01-23

PRIOR FILING DATE: 2004-01-24

NUMBER OF SEQ ID NOS: 277

SOSTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Agensys, Inc.
APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Baitano, Arthur B.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
ITILE OF INVENTION: Nucleic Acids and Corresponding Proteins
ITILE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
ITILE OF INVENTION: Cancer
ITILE OF INVENTION: Cancer
ITILE OF INVENTION: USER 254PlD6B Useful in Treatment and Detection of
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT APPLICATION NUMBER: US/04-01-23
FRICR PAPLICATION NUMBER: US/04-01-24
NUMBER OF SEO ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 265
LENGTH: 24
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1.5%; Score 16; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 265, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
1 MAPPTGVLSSLLLLVTIA 18
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Best Local Similarity 100.
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-764-390-265
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; ORGANISM: Homo sapiens
US-10-764-390-43
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US-10-764-390-265
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Taltano, Arthur B.
APPLICANT: Taltano, Arthur B.
APPLICANT: Taltano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
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APPLICANT: Steven B. Kanner

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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US60/442,526
FRIOR APPLICATION NUMBER: US60/442,526
FRIOR APPLICATION NUMBER: US60/442,526
FRIOR APPLICATION OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 262
LENGTH: 29
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Pred. No. 4.2e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                           Sequence 262, Application US/10764390; Publication No. US20040214212A1; GENERAL INPORMATION: APPLICANT: Agensys, Inc. APPLICANT: Raitano, Arthur B. APPLICANT: Takobovits, Aya APPLICANT: Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 268, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION:
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100.0%; Pre
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20 CARKQCSEGRIYSN 33
                                                                                     11 CARKÓCSEGRIYSN 24
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Best Local Similarity 100.(
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-390-262
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US-10-764-390-268
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0.8%; Score 9; DB 1
100.0%; Pred. No. 1.7
tive 0; Mismatches
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Sequence 46, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
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                                                                           Query Match 0.8
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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  ; ORGANISM: Homo sapiens
US-10-764-390-45
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1 GVLSSLLLL 9
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| APPLICANT: Raitano, Arthur B. |
| APPLICANT: Raitano, Arthur B. |
| APPLICANT: Raitano, Arthur B. |
| APPLICANT: Challita-Eid, Pia M. |
| APPLICANT: Challita-Eid, Pia M. |
| APPLICANT: Ge, Wangmao |
| APPLICANT: Seven B. Kanner |
| APPLICANT: Seven B. Kanner |
| APPLICANT: Seven B. Kanner |
| APPLICANT: Seven B. Entitled 254PlD6B Useful in Treatment and Detection of TITLE OF INVENTION: Butitled 254PlD6B Useful in Treatment and Detection of TITLE OF INVENTION: Cancer |
| TITLE OF INVENTION: Cancer |
| TITLE OF INVENTION: Cancer |
| FILE REFERENCE: 51158-20081.00 |
| CURRENT APPLICATION NUMBER: US/10/764,390 |
| CURRENT FILING DATE: 2004-01-24 |
| NUMBER OF SEQ ID NOS: 277 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Saitano, Arthur B.
APPLICANT: Jacobovits, Aya
APPLICANT: Jacobovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Juan J. Perez-Villar
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION WINNER: US(10/764,390
CURRENT APPLICATION NUMBER: US(10/764,390
CURRENT APPLICATION NUMBER: US(0/442,526
FRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 9
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                                                        Gaps
     Length 29;
                                                   0; Indels
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0.8%; Score 9; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
Query Match
1.3%; Score 14; DB 16; L
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 45, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                      US-10-764-390-44; Sequence 44, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION:
                                                                                                    128 GIWGDSPEDIRKDL 141
                                                                                                                                                     1 GIWGDSPEDIRKDL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-10-764-390-44
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of
TITLE OF INVENTION: Solvantial Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven Steven
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APPLICANT: Raitano Arthur B.
APPLICANT: Takobovits, Aya
APPLICANT: Takobovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Cancer
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TITLE OF INVENTION: Cancer
FILE REPRENENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
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No. 1.78+06; Indels
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RESULT 13
US-10-764-390-51
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                                                                                                                            TYPE: PRT
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APPLICANT: Agensys, Inc.

APPLICANT: Raitano, Arthur B.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Ge, Wangmao

APPLICANT: Ge, Wangmao

APPLICANT: Faris, Mary

APPLICANT: Faris, Mary

APPLICANT: Faris, Mary

APPLICANT: Geven B. Kanner

APPLICANT: Geven B. Kanner

APPLICANT: Steven B. Entitled 254PlD6B Useful in Treatment and Detection of

TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

FILE REFERENCE: 51158-20081.00

CURRENT APPLICATION NUMBER: US/10/764,390

CURRENT FILING DATE: 2004-01-23

PRIOR FILING DATE: 2004-01-24

NUMBER OF SEQ ID NOS: 277

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 9
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j Sequence 49, Application US/10764390

j Sequence 49, Application US/10764390

j Sequence 49, Application No. US20040214212A1

j GENERAL INFORMATION:

j APPLICANT: Raitano, Arthur B.

j APPLICANT: Ge, Wangmao

j APPLICANT: Farith, Maya

APPLICANT: Farith, Maya

APPLICANT: Farith, Mary

j APPLICANT: Farith, Mary

j APPLICANT: Farith, Mary

j APPLICANT: Brith, Mary

j APPLICANT: Brith Mary

j TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of

j TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of

j TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of

j TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of

j CURRENT APPLICATION NUMBER: US/10/764,390

j CURRENT FILING DATE: 2004-01-23

j PRIOR APPLICATION NUMBER: US60/442,526
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100.0%; Pred. No. 1.7e+06;
iive 0; Mismatches 0; Indels
                                                                                                                                                    Query Match 0.8%; Score 9; DB 16; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 9; Conservative
                                                TYPE: PRT
ORGANISM: Homo sapiens
US-10-764-390-47
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ORGANISM: Homo sapiens
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SEQ ID NO 47
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Brish Mary
APPLICANT: Faris, Mary
APPLICANT: Brish Mary
APPLICANT: Brish Mary
APPLICANT: Brish Mary
APPLICANT: Cancer
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT FILING DATE: 2004-01-23
PRIOR PILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US60/442,526
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SSPTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
FILE REFERENCE: 51158-20081.00
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0.8%; Score 9; DB 16; Le
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 9
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Publication No. US20040214212A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION:
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US-10-764-390-49
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US-10-764-390-52
Sequence 52, Application US/10764390
Sequence 52, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: General Avanama
APPLICANT: General Andrew
APPLICANT: General Andrew
APPLICANT: General Andrew
APPLICANT: General Andrew
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APPLICANT: General Andrew
TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
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; APPLICANT: Raitano, Arthur B.; APPLICANT: Challitane, Aya; APPLICANT: Challitane, Aya; APPLICANT: Challitane, Applicant: Challitane, Applicant: Raitano, Arthur B.; APPLICANT: Ge, Wangmao; APPLICANT: Steven B. Kanner; APPLICANT: Steven B. Kanner; APPLICANT: Usan J. Perez-Villar; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
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Outlier 100.0%; Pred. No. 1.7e+06;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 9
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-764-390-52
                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-10-764-390-51
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
044446947
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78, Appl
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205, App
320, App
168, App
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Sequence 78,
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-889-136-6
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                          Sequence:
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                                                                                                                                   Run on:
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28 6 0 6 22 1 18:09-98-916-11 Sequence 11, Appl 20 6 0 6 22 1 18:09-913-166-4 Sequence 15, Appl 20 6 0 6 22 1 18:09-913-166-4 Sequence 15, Appl 20 6 0 6 22 1 18:09-911-14 Sequence 15, Appl 20 6 0 6 22 1 18:09-911-14 Sequence 17, Appl 20 6 0 6 22 1 18:09-911-14 Sequence 17, Appl 20 6 0 6 22 1 18:09-911-14 Sequence 17, Appl 20 6 0 6 22 1 18:09-911-14 Sequence 17, Appl 20 6 0 6 22 1 18:09-911-14 Sequence 17, Appl 20 6 0 6 22 1 18:09-911-14 Sequence 17, Appl 20 6 0 6 22 1 18:09-911-14 Sequence 17, Appl 20 6 0 6 22 1 18:09-911-14 Sequence 17, Appl 20 6 0 6 25 1 18:09-911-14 Sequence 22, Appl 20 6 0 6 25 1 18:09-911-14 Sequence 22, Appl 20 6 0 6 25 1 18:09-911-14 Sequence 22, Appl 20 6 0 6 25 1 18:09-911-14 Sequence 22, Appl 20 6 0 6 25 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 25 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 25 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 25 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20 1 18:09-911-14 Sequence 21, Appl 20 6 0 6 20
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TYPE: PRT
ORGANISM: Homo sapiens
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US-08-096-762-205
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                     US-09-261-855-14
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US-09-001-984C-78

Sequence 78, Application US/09001984C

Sequence 78, Application US/09001984C

Sequence 78, Application US/09001984C

GENERAL INFORMATION:

APPLICANT: Laal, Suman

APPLICANT: Belisle, John T

TITLE OF INVENTION: BARLY DETECTION OF WYCOBACTERIAL DISEASE

TITLE REFERENCE: NVV-011

CURRENT APPLICATION NUMBER: US/09/001,984C

CURRENT FILING DATE: 1997-12-31

PRIOR PILING DATE: 1997-12-31

PRIOR PILING DATE: 1996-12-31

NUMBER OF SEQ ID NOS: 106

SOFTWARE: Patentin Ver. 2.1
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Fatent No. 6506384
Fatent No. 6506384
GENERAL INFORMATION:
APPLICANT: Lal, Suman
APPLICANT: Ealisle, John TITLE OF INVENTION:
TITLE OF INVENTION: EARLY DETECTION OF WYCOBACTERIAL DISEASE
FILE REFERENCE: 32004-169276
CURRENT APPLICATION NUMBER: US/09/396,347F
CURRENT FILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.1
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                                     0.6%; Score 6; DB 2; Length 7;
100.0%; Pred. No. 4.1e+05;
iive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-78
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; TYPE: PRT
ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-396-347F-78
                                     Query Match 0.6
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                      222 ASTPAP 227
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US-09-396-347F-78
US-08-666-473-53
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LENGTH: 10
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Sequence 14, Appgication US/09261855A

SEQUENCE 17, Appgication US/09261855A

SEQUENCE 17, Appgication US/0926185A

SEQUENCE 18029.

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us-10-764-390-3.011.rai

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FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
IOR APPLICATION:
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STRANDEDNESS:
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pactent No. 6255458

GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: California
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 2-JUL-1993
CLASSIFICATION NUMBER: US 08/053,131
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 26-APR-1993
PRIOR APPLICATION NUMBER: US 07/990,668
FILING DATE: 3-JUN-1992
PRIOR APPLICATION NUMBER: US 07/990,668
FILING DATE: 3-JUN-1992
PRIOR APPLICATION NUMBER: US 07/991,068
FILING DATE: 3-JUN-1992
PRIOR APPLICATION NUMBER: US 07/813,408
FILING DATE: 3-JUN-1992
PRIOR APPLICATION NUMBER: 30,233
PRIOR APPLICATION NUMBER: 14643-9-4
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELEPHONE: 415-326-2420
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LINFORMATION POR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LELEBOTH: 2 maino acide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
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US-09-042-353-320
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0.6%; Score 6; DB 3; Le:
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 08/165,699

PRIOR APPLICATION NUMBER: US 08/165,699

PRIOR APPLICATION NUMBER: US 08/165,699

PRIOR APPLICATION NUMBER: US 08/209,741

PRIOR APPLICATION NUMBER: US 08/352,322

PRIOR APPLICATION NUMBER: US 08/352,322

PRIOR APPLICATION NUMBER: US 08/352,322

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,404

PRILING DATE: U-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463

FILLING DATE: U-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463

FILLING DATE: U-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/758,417

FILLING DATE: U-DCT-1996

PRIOR APPLICATION NUMBER: US 08/758,417

FILLING DATE: U-DCT-1996

PRIOR APPLICATION NUMBER: US 08/758,417

FILLING DATE: U-DCC-1996

PRIOR APPLICATION NUMBER: 36,429

FILLING DATE: U-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: APPLICATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 014643-009040US

TELEPHONE: (415) 576-0300

TELEPHONE: (415) 576-0300
CLASSIFICATION: 800
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-UN-1992
PRIOR APPLICATION NUMBER: US 07/900,860
FILING DATE: 26-DEC-1992
PRIOR APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION NUMBER: US 08/056,762
FILING DATE: 22-UUL-1993
PRIOR APPLICATION NUMBER: US 08/056,762
FILING DATE: 22-UUL-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/155,301
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US-09-044-718-8
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                                        Sequence 168, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 02-Dec-1996
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                           STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-0CT-1996
FILING DATE: 10-0CT-1996
APPLICATION NUMBER: US 08/54,404
FILING DATE: 10-0CT-1995
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 09-MAR-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 01-DEC-1993
APPLICATION NUMBER: US 08/16,739
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,301
FILING DATE: 22-ULL-1993
APPLICATION NUMBER: US 08/056,762
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INPORMATION:
NAME: SGRAFING ANDRER: 41,303
REGISTRATION NUMBER: 41,303
REGISTRATION NUMBER: 41,303
REGISTRATION NUMBER: 41,303
REGISTRATION NUMBER: 41,303
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 168:
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TELEFAX: (415) 576-0300
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                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 417
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
RESULT 8
US-08-758-417A-168
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100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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100.0%; Pred. No. 2.5
tive 0; Mismatches
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APPLICANT: ROSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: VOGEL, KULT
APPLICANT: VOGEL, KULT
APPLICANT: WORGE, KULT
APPLICANT: WORGE, KULT
APPLICANT: WORGE, WATHUS
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: US/044,718
PRIOR APPLICATION NUMBER: BP 97810175.6
PRIOR FILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PATEUR OF SEQ ID NOS: 82
SEQ ID NOS: 82
                                                                APPLICANT: COSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: vooel, Kurt
APPLICANT: VOOEL, Kurt
APPLICANT: WISS, Markus
APPLICANT: WOOEL, Kurt
APPLICANT: WOOEL, Kurt
APPLICANT: WOOEL, Kurt
APPLICANT: WOOEL, Kurt
APPLICANT: WOOEL, Kurt
APPLICANT: WOOEL, Kurt
APPLICANT: WOOEL, Kurt
APPLICANTON: MODIFIED PHYTASES
CURRENT FILING DATE: 1996-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Talaromyces thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Talaromyces thermophilus
Sequence 8, Application US/09044718
Patent No. 6391605
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10062848 Patent No. 6734004
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Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conserv
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SLLLLV 7
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Patent No. 6838254
GENERAL INFORMATION:
APPLICANT: Raymond HAMERS-CASETERMAN
APPLICANT: Serge V. M. MUYLDERWANS
APPLICANT: Serge V. M. WUYLDERWANS
APPLICANT: Serge V. M. SERENCEN
APPLICANT: Cornelis T. VERRIPS
TITLE OF INVENTION: Production of antibodies or (functionalized)
TITLE OF INVENTION: fragments thereof derived from heavy chain immunoglobulins
                                                                                                        APPLICANT: Cecile HAMERS-CASETERMAN
APPLICANT: Serge V. M. WIVIDERMANS
APPLICANT: Leon G. J. FRENKEN
APPLICANT: Cornelis T. VERRIPS
APPLICANT: Cornelis T. VERRIPS
TITLE OF INVENTION: PROduction of antibodies or (functionalized)
TITLE OF INVENTION: Camelidae
TITLE OF INVENTION: of Camelidae
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. 2.7e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 6; DB 4
100.0%; Pred. No. 2.7
tive 0; Mismatches
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APPLICATION NUMBER: PCT/EP94/01442
FILING DATE: 28-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BPO 93202079.5
FILING DATE: 15-JUL-1993
PRIOR APPLICATION NUMBER: BPO 93201454.1
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BPO 93201454.1
FILING DATE: 29-APR-1993
FILING DATE: 29-APR-1993
FILING DATE: 29-APR-1993
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,871A
FILING DATE: 29-JAN-1996
                Sequence 41, Application US/08537871A Patent No. 6838254 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
                                                                                        : Raymond HAMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Then 6; Conservative
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LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein IMMEDIATE SOURCE:
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US-08-537-871A-41
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US-08-537-871A-45
US-08-537-871A-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08347198A
Patent No. 5747046
GENERAL INFORMATION:
APPLICANT: WINN, Edward A.
APPLICANT: SMITH, Trevor S.
TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNGENS
ITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNGENS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESTANDENLE ADDRESSES:
STREET: 655 FIfteenth Street, N. W., Suite 330 - G
STREET: Street Lobby
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
TITLE OF INVENTION: Of Camelidae
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 93201239.6
ILING DATE: 29-APR-1993
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDENNESS: single
                                                                                                                                    COUNTRY: USA
ZIP: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,871A
FILING DATE: 29-JAN-1996
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
RAPLICATION NUMBER: PCT/EP94/01442
FILING DATE: 28-APR-1994
PRIOR APPLICATION NUMBER: BPO 93202079.5
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
PLING APPLICATION DATA:
PLING APPLICATION DATA:
APPLICATION NUMBER: EPO 93201454.1
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Matches 6; Conserv
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MOLECULE TYPE:
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US-08-347-198A-11
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Sequence 35, Application US/08335844A

Sequence 35, Application US/08335844A

Patent No. 606503

APPLICANT: GRAHAM, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, BDWARD ALBERT
APPLICANT: MUNN, DAVID PATRICK
APPLICANT: NUNX, DAVID PATRICK
APPLICANT: NUNX, DAVID PATRICK
APPLICANT: NUNX DAVID PATRICK
APPLICANT: NUNX DAVID PATRICK
APPLICANT: NUNX SUSAN BLIZABETH
APPLICANT: NUNXTION: NECOMBINANT DNA MOLECULES ENCODING
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
CORRESPONDES: 73
CORRESPONDES: 73
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CORE
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100.0%; Pred. No. 2.9e+02;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC Compatible
COMPUTER: Elem PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,844A
FILING DATE: 09-JAN-1995
CLASSIFICATION ADATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
ATONNEY/AGENT INFORMATION:
NAME: WALKER, BATDARA W.
REGISTRATION NUMBER: 35,400
REFERBNICE/DOCKET NUMBER: 35,400
REFERBNICE/DOCKET NUMBER: 1181-223A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                              100.0%; Pr
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SEQUENCE CHARACTERISTICS:
      53:
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                                                                       17 amino acids
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                    single
                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: Protein US-08-248-839C-53
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserva
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US-08-248-839C-53
Sequence 53, Application US/08248839C
PAPELICANT: McConnell, David
APPLICANT: McConnell, David
APPLICANT: O'Kane, Charles
TITLE OF INVENTION: A Gene Expression System
NUMBER OF ENGURENCE: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58437020 No. 5843702th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
CONNTR: USA
CONNTR: USA
CONNTR: USA
TILOTA-640 NA
SDIW TYPE: Diskette
CONNTRES: FactSEQ for Windows Version 2.0
CONNTRES: PastSEQ for Windows Version 2.0
CONNTRES: STATES OF STATES OF WINDOWS TO WINDOWS TILOTATION NUMBER: 35-MX-1994
CLASSIFICATION NUMBER: 35-MX-1994
CLASSIFICATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 3614.14-US
TELEPHONE: 212-867-0123
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
                    FILING DATE: 21-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/020,526
FILING DATE: 22-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/761,749
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00416
FILING DATE: 19-MAR-1990
PRIOR APPLICATION NUMBER: GB 89906156.8
FILING DATE: 17-MAR-1989
APPLICATION NUMBER: GB 89906156.8
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICAC.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 36,105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-580
APPLICATION NUMBER: US/08/347,1982
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SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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Best Local Similarity 100.
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TYPE: amino acid
STRANDEDNESS: single
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·	ALIGNMENTS	18 AA.	ed) sequence update) annotation update) ent).	Craniata, Vertebrata; Catarrhini, Hominidae;	4; DOI=10.1074/jbc.274.10. Kim K.S.; and extensive 5' upstream ivation, are necessary for the human norepinephrine	1999). E8333908ED35CD2D CRC64	re 6; DB 2; Len ed. No. 1.1e+03; Mismatches 0;		22 AA.  puence update)  cotation updat  cagment).  tta; Vertebrat  sgnathi; Murid  SOI=10.1074/jb  brown T.J., Dx  on in the muri
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Swelsen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ316290; CAC87135.1; -.
NON TER
SRQÜENCE 24 AA; 2669 MW; 1942CFC2489CI77F CRC64;
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SWellen W.T., Voorter C.E., van den Berg-Loonen B.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ316288; CAC87133.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Leucocyte antigen (Fragment).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0004967; F:glucagon receptor activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Swelsen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Swelsen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ316291; CAC87136.1; -.
NON TER 24 24
SEQUENCE 24 AA; 2669 MW; 1942CFC2489C177F CRC64;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databasee.
EMBL; AJ316292; CAC87137.1; -.
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22 AA; 2526 MW; 2C5BF53DCCD425C9 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Leucocyte antigen (Fragment).
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system is enhanced by elimination of
J. Biol. Chem. 276:21489-21499(2001)
EMBL; AF338224; AAK63043.1; -.
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24 AA; 2669 MW; 1942CFC2489C177F CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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tive 0; Mismatches 0; Indels
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ316287; CAC87132.1; -.
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Swelsen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databasee.
EMBL; AJ316286; CAC87879.1; -...
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Swelsen W.T., Voorter C.E., van den Berg-Loonen B.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ31628; CAC878.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Leucocyte antigen (Fragment).
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Leucocyte antigen (Fragment).
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                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                    Name=HLA-B;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Swelgen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ429190; CAD22131.1; -.
NON TER 24 22
SEQÜENCE 24 AA; 2669 MW; 1942CFC2489CI77F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 6; DB 2; Length 24;
100.0%; Pred. No. 1.5e+03;
Artive 0; Mismatches 0; Indels
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TISSUBE-PETIPHERAL blood;
Swelsen W.L. Voorter C.E., van den Berg-Loonen B.M.;
Swelsen W.V. Voorter C.E., van den Berg-Loonen B.M.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ417674; CAD10406.1; -.
NON TER
SEQUENCE 24 AA; 2669 MW; 1942CFC2489C177F CRC64;
                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Leucocyte antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
MHC class I antigen (Fragment).
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24 AA.
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Best Local Similarity 100.(
Matches 6; Conservative
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PRELIMINARY;
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Amphibian defense peptide; Antibiotic; Direct protein sequencing;
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Name=UL15;
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MEDLINE=94139686; PubMed=8306981;

Mor A., Nicolas P.,

"Isolation and structure of novel defensive peptides from frog skin.";

Bur. J. Blochem. 219:145-154(1994).

-!- FUNCTION: Possesses a potent antimicrobial activity against bacteria, fungi and protozoa. Probably acts by disturbing membrane functions with its amphipatic structure.

-!- SUBCELBULAR LOCATION: Secreted.

-!- TISSUE SEPECIFICITY: Skin.

-!- SIMILARITY: BLOGATIONS Skin.

-!- SIMILARITY: Bubganily.
                                                                                                                                                                                                                MEDLINE=99259579; PubMed=10327595; DOI=10.1016/S0305-0491(98)10144-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                       -1- FUNCTION: Hemocyanins are copper-containing oxygen carriers occurring freely dissolved in the hemolymph of many mollusks and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNS4 PHYSA STANDARD; PRT; 27 AA.

B80280;

CHOI-FEB-1994 (Rel. 28, Created)

O1-FEB-1994 (Rel. 28, List sequence update)

O5-JUL-2004 (Rel. 44, Last annotation update)

O5-JUL-2004 (Rel. 47, Last annotation update)

Phyllomedusa sauvagei (Sauvage's leaf frog).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000896; Hemocyanin.
InterPro; IPR00227; Tyrosinase.
PROSITE; PS00209; HEMOCYANIN 1; PARTIAL.
PROSITE; PS00497; TYROSINASE 1; PARTIAL.
PROSITE; PS00497; TYROSINASE 1; PARTIAL.
COPPER; DS00498; TYROSINASE 2; PARTIAL.
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                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Extracellular.
-i- TISSUE SPECIFICITY: Hemolymph.
-i- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin
                                                                                                                      Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Astacidea,
Nephropoidea, Nephropidae, Homarus.
                                                                                                                                                                                                                              Stoeva S., Dolashka P., Hristova R., Genov N., Voelter W., "Subunit composition and N-terminal analysis of arthropod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6%; Score 6; DB 1; Length 26; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 26 26 28 2903 MW; 7F3549875A638D61 CRC64;
                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homarus americanus (American lobster).
                  26 AA
                                                                                                                                                                                                                                                                         Biochem. Physiol. 122B:69-75(1999)
                  PRT;
                  STANDARD;
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MEDLINE=92024477; PubMed=1656627; DOI=10.1016/0168-1702(91)90064-3; MEDLINE=92024477; PubMed=1656627; DOI=10.1016/0168-1702(91)90064-3; Dolan A., Arbuckle M., McGeoch D.U.; Sequence analysis of the splice junction in the transcript of herpes simplex virus type 1 gene UII5."; Virus Res. 20:97-104(1991). EMBL; S62788; AAB20055.1; -. EMBL; S62788; AAB20055.1; -. InterPro; IPR03323; P:DNA packaging; IEA. InterPro; IPR03499; DNA pack N. Franscript of Promise Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Profits of Prof
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"Increased water permeability across the blood-gas barrier in rabbit lungs in the first 24 hours after birth.";
J. Clin. Invest. 0:0-0(1997).
EMBL; AF000313; AAB94410.1; -.
NON TER 1 1 31
SEQÜENCE 31 AA; 3525 MW; F80D65C92838FA92 CRC64;
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                     DB 1; Length 27;
Fungicide; Multigene family.
SEQUENCE 27 AA; 2779 MW; 43C94D2DC19721A8 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-actin (Fragment)
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                     0.6%; Score 6; DB 1; Ler
100.0%; Pred. No. 1.6e+03;
rative 0; Mismatches 0;
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05-JUL-2004 (TrEMBLrel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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0; Gaps Query Match 0.6%; Score 6; DB 2; Length 31; Best Local Similarity 100.0%; Pred. No. 1.8e+03; Matches 6; Conservative 0; Mismatches 0; Indels

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136 DIRKDL 141 |||||| 24 DIRKDL 29

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Search completed: October 12, 2005, 10:25:21 Job time : 69 secs

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October 12, 2005, 10:19:24; Search time 21 Seconds (without alignments) 4911.637 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                  Run on:
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1 MAPPIGVLSSLLLLVTIAGC......VSMNGSIRNGASFSYCSKDR 1072 OLIGO Gapop 60.0 , Gapext 60.0 US-10-764-390-3 Perfect score: Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

7756 Total number of hits satisfying chosen parameters:

0

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 35

Post-processing: Listing first 45 summaries

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SUMMARIES	Description	anslatio	IS1/cat protein -		variant surface gl	lacto			glutathione peroxi	hypothetical prote					Ig heavy chain J	T-cell receptor	T-cell receptor		26						45/47K antigen -	protein-tyrosine	d gi		T-ce	T-complex protein
MOS.	۵	855937	153186	G60529	A21440	A47364	PT0255	PT0319	A38929	809395	847377	S29878	S27140	S26791	PS0382	G41299	F28587	PS0383	D58501	C37520	S26747	S26744	124687	PS0384	A49237	824780	A25941	139461	ന	28
	DB	7	~	~	7	7	7	~	~	~	~	7	~	~	~	N	N	N	N	~	7	~	~	~	7	7	N	4	~	~
	อี	32	33		œ	10	12	12	13	13	13	14	14	15	15	15	15	16	16	17	17	17	17	. 17	17	18	18	18	19	19
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		1	7	m	4	2	9	7	60	on.	10	11	12	13		15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig heavy chain CRD cytochrome P450 PB malate dehydrogena equinatoxin 1C - s 2-halobenzoate 1,2 d'TDPglucose 4,6-de coenzyme F420 hydr tenebrosin B - sea RNA-binding protei duodenase - bovine 110% ATPase, intes ribosomal protein alpa-1-antichymot Ta heavy chain D.T	kinetoplast DNA-as hemocyanin 1 - edi
PT0332 A60822 S04961 PC1151 B44920 B44835 S6935 B46174 A6174 A61487 A61487 S29858 I54568 PH1333	D47256 A60529
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~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	444

## ALIGNMENTS

	RESULT 1
	translation initiation factor eIF-4E - fruit fly (Drosophila melanogaster) (fragments)
	C;Species: Drosophila melanogaster C;Date: 27-Oct-1995 #sequence revision 03-Nov-1995 #text change 09-Jul-2004
	C;Accession: S55937
	R;Hernandez, G.; Sierra, J.M.
	Biochim. Biophys. Acta 1261, 427-431, 1995
_	A, Title: Translation initiation factor eIF-4E from Drosophila: cDNA sequence and express
	A; Reference number: S55936; MUID: 95260867; PMID: 7742371
	A;Accession: S55937
	A;Status: preliminary
	A; Molecule type: protein
	A;Residues: 1-8;9-27;28-32 <her></her>
_	A;Cross-references: UNIPROT:Q7M4E6
_	C;Genetics:
	A;Gene: FlyBase:Bif4F
	A;Cross-references: FlyBase:FBgn0013947
	C; Superfamily: translation initiation factor eIF-4E
	Ouery Match 0.6%; Score 6; DB 2; Length 32;
_	Best Local Similarity 100.0%; Pred. No. 2.8e+02;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

307 PPTSAA 312 PPTSAA 26 21 a ð

1S1/Cat protein - Escherichia coli (fragment)

C;Species: Bscherichia coli

C;Species: Bscherichia coli

C;Species: Bscherichia coli

C;Species: Bscherichia coli

C;Species: Bscherichia coli

C;Species: Bscherichia coli

C;Species: Bscherichia coli

C;Species: Bscherichia coli

C;Species: Bscherichia coli

S;Stacession: 153186; Bickle, T.A.

A;Title: Phenotypic reversion of an IS1-mediated deletion mutation: A combined role for A;Reference number: 153186; MUID:84236045; PMID:6329702

A;Accession: I55186

A;Accession: I55186

A;Accession: I55186

A;Accession: I6885

A;Cross-references: UNIPROT:Q52315; GB:M24180; NID:g151758; PIDN:AAA26059.1; PID:g151759

A;Accession: Bceliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA A;Residues: 1-18,'G' <RE2> A;Cross-references: GB:M24181; NID:g151760; PIDN:AAA26060.1; PID:g151761 Query Match 0.6%; Score 6; DB 2; Length 33; Best Local Similarity 100.0%; Pred. No. 2.9e+02;

6; Conservative

Matches

867 IVFYVQ 872

ò g

15 İVPYVQ 20

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PT0255

Ig heavy chain CRD3 region (clone 2-115B) - human (fragment)

Ig heavy chain CRD3 region (clone 2-115B) - human (fragment)

Ig heavy chain gapless (man)

C;Species: None sapless (man)

C;Accession: PT0255

C;Accession: PT0255

If you wed: 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and 3

A;Reference number: PT0222; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Space: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C.Accession: Pr0319
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A.Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J.
A.Reference number: PT0222; MUID:91108337; PMID:1899102
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R;Gettins, P.; Dyal, D.; Crews, B.
R;Gettins, P.; Dyal, D.; Crews, B.
A;Ach. Biochem. Biophys. 294, 511-518
A;Title: Selenium-dependent glutathione peroxidases from ovine and bovine erythrocytes c. A;Reference number: S21712; MUID:92231574; PMID:1567207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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h 0.5%; Score 5; DB 2; Length 10; Similarity 100.0%; Pred. No. 1.1e+03; 5; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.3e+03;
ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain CRD3 region (clone 6-127) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reaidues: 1-12 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Experimental source: B lymphocyte
C, Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 100.
Matches 5; Conservative
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-13 <GET>
        Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                           392 TLNLS 396
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A; Residues: 1-12 < YAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Cherax destructor (yabby)
C.Date: 19-Mar-1993 #text_change 09-Jul-2004
C.Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C.Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C.Date: 19-Mar-1993 #sequence 18-Mar-1993 #text_change 09-Jul-2004
R.Neuteboom, G.Sierdsema, S.J.; Beintema, J.J.
Comp. Blochem. Physiol. B 94, 587-592, 1989
A.Tatle: The relationship between N-terminal sequences and immunological characterizatic
A.Accession: G60529
A.Fatus: preliminary
A.Rotesule type: protein
A.Molecule type: protein
A.Rotesule type: protein
A.Residues: 1-35 < NBU>
A.Cross-references: UNIPROT:P83173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
A47364
placental lactogen-I precursor - mouse (fragment)
cl.Species: Mus sp. (mouse)
C.Species: Mus sp. (mouse)
C.Species: Mus sp. (mouse)
C.Species: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C.Species: Mus sp. (mouse)
C.Species: Mus sp. (mouse)
C.Species: Mus sp. (sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus sp. Mus s
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C; Species: Trypanosoma brucei
C; Species: Trypanosoma brucei
C; Species: Trypanosoma brucei
C; Species: Trypanosoma brucei
C; Accession: A21440
R; Parsons, M.; Nelson, R.G.; Watkins, K.P.; Agabian, N.
Cell 38, 309-316, 1984
A; Title: Trypanosome mRNAs share a common 5' spliced leader sequence.
A; Reference number: A90853; MuID:84282716; PMID:6088073
A; Reference number: A90853; MuID:84282716; PMID:6088073
A; Residues: 1-8 - PRR>
A; Residues: 1-8 - PRR>
A; Residues: 1-8 - PRR>
A; Cross-references: UNIPROT:P22225; GB:K02195; NID:g162150; PID:g162151
C; Keywords: glycoprotein
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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             Indels
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                                                                                                                                                                                                                                                                                                  RESULT 3
G60529
hemocyanin M3' - crayfish (Cherax destructor) (fragment)
             ;
0
             Mismatches
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6; Conservative

Best Local Similarity Matches 6; Conserv

Query Match

900 FLLFKV 905

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17 FLLFKV 22

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Gaps

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C;Accession: S27140
R;Keaveney, M.; Klug, J.; Gannon, F.
Naby Seq. 2, 347-358, 1992
A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene A;Reference number: S27140; MUID:93075998; PMID:1476547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (N63P2) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 02-Aug-1996 #text_change 20-Jun-2000
C;Accession: 525791; S19879
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Riwr. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami A;Reference number: S26786; MUID:92111632; PMID:1730251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross references: EMBL:X61022; NID:g32791; PIDN:CAA43356.1; PID:g1335124; EMBL:X61234; C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain J region 2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 06-Jun-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Homo sapiens (man)
C.Spate: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44319.1; PID:g31202
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100.0%; Pred. No. 1.5e+03;
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Best Local Similarity 100.0%; Pred. No. 1.5
Matches 5; Conservative 0; Mismatches
                       A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 < LIYT>
A;Cross-references: UNIPROT:Q7M0G4
C;Keywords: hydrolase
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Best Local Similarity 100.0
Matches 5; Conservative
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A; Residues: 1-14 < KEA>
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  A;Accession: S29878
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"Species: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997

C;Accession: S09395

R;Gisselmann, G:, Sewing, S:, Madsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Holtk

R;Gisselmann, G:, Sewing, S:, Mudsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Holtk

BMO, G:, S1559-2364, 1989

A;Fitle: The interference of truncated with normal potassium channel subunits leads to a

A;Reference number: S09395

A;Accession: S09395

A;Accession: S09395

A;Accession: Ribaninary

A;Molecule type: mRNA

A;Residues: 1-13 <GIS>
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submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47377
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A;Residues: 1-13 <LEH>
A;Crese -references: EMB::Z35706; NID:g527505; PIDN:CAA84775.1; PID:g527506
C;Keywords: T.cell receptor
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tive 0; Mismatches 0; Indels
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ative 0; Mismatches 0;
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0.5%; Score 5; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0;
A;Cross-references: UNIPROT:Q7M355
C;Superfamily: glutathione peroxidase
C;Keywords: oxidoreductase
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A, Accession: S47377
A, Status: preliminary
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RESULT 15

G41299

C; Cell receptor alpha chain precursor J region (39) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 05-Nov-1999
C; Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 05-Nov-1999
R; Usersion: G41299
R; Usersion: G41299
A; Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheumatch A; Reference number: A41299; MUID:92020887; PMID:1656449
A; Recession: G41299
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-15 < UEM>A; Residues: 1-15 < UEM>A; Residues: T-cell receptor
C; Keywords: T-cell receptor
C;Accession: PS0382
R;Lang, P.; Mocikat, R.
Rene 102, 261-264, 1991
A;Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and A;Reference number: JH0666; MUD:91340162; PMID:1908401
A;Reference number: JH0666; MUD:91340162; PMID:1908401
A;Residues: J-15 claNs
A;Residues: 1-15 claNs
A;Cross-references: EMBL:X56791
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
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Minimum Maximum Database :

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypoptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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23-AUG-2000; 2000US-00649167
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 WPI; 2001-639362/73.
N-PSDB; AAS86253.
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ADRO0722
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ADRO0767
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ADRO0769
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ADRO06683
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ADR00775
ADR00784
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geneseqp2003as:*
geneseqp2003bs:*
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geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
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seq length: 35
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of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New 254PID6B BIRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PID6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a 254PlD6B small interfering RNA (siRNA)
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
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                                                                                                                                                                                                                                                            DB 4; Length 19; 2.7e-09;
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                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                          1.7%; Score 18;
.00.0%; Pred. No.
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Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 254P1D6B peptide SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR00632 standard; peptide; 16 AA.
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                          Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of F1; (5) detecting, in a sample, the presence of a 254PloBb-related protein or a 254PloBb-related protein or a 254PloBb-related protein or a 254PloBb-related protein or a catus of a cell that expresses a protein of F1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of F1; and cypress the protein of P1. 254PloBb has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PloBb gene is located on chromosome 6p22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PlD6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises,
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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254PID6B-related protein; cytostatic; gene therapy; cancer; human;
254PID6B v.3; chromosome 6.
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                                                                                                                                                                                                                                                                                                                                                                                    Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                  Score 16; DB 8; Le
Pred. No. 2.1e-07;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 13; SEQ ID NO 265; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 254P1D6B v.3 peptide SEQ ID NO:265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR00854 standard; peptide; 24 AA.
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 NNAVDYPPVANAGPNH
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
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Perez-Villar JJ, Faris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-580991/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004067716-A2
                                                                                                                                                                                                                                                                                                                                                Sequence 16 AA;
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consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pt. see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596, or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein cany of the test 90, 91, 92, 33, 94, 95, 96, 97, 98, or 93# homologous or identical to an entire amino acid sequence of P1; (2) a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide that encodes the protein of 10 a composition comprising a polymucleotide certing, in a sample, the presence of a 254PlD68-related protein or 254PlD68-related polymucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above; (9) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD68 has cytostatic activity, and can be capted and detecting cancer. The present sequence represents a chuman 254PlD68 v.3 peptide, which is used in the exemplification of the present invention. The human 254PlD68 gene is located on chromosome 6p22.
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Sequence 24 AA;

ö Gaps ö 1.3%; Score 14; DB 8; Length 24; 100.0%; Pred. No. 2.6e-05; tive 0; Mismatches 0; Indels 14; Conservative Query Match Best Local Similarity Matches

20 CARKQCSEGRIYSN 33 ò 셤

11 CARKQCSEGRIYSN 24

ADR00851 standard; peptide; 29 AA. ABSULT 4
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(first entry) 04-NOV-2004 ADR00851;

254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.2; chromosome 6. Human 254P1D6B v.2 peptide SEQ ID NO:262.

Homo sapiens

WO2004067716-A2.

12-AUG-2004.

24-JAN-2003; 2003US-0442526P.

23-JAN-2004; 2004WO-US001965.

(AGEN-) AGENSYS INC.

Ge ₩; Kanner SB, Raitano AB, Jakobovits A, Challita-Eid PM, Perez-Villar JJ, Faris M;

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 13; SEQ ID NO 262; 345pp; English.

New 254P1D6B siRNA composition comprising a double stranded siRNA that

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Challita-Eid PM,

Jakobovits A,

Kanner SB, Raitano AB, Ja Perez-Villar JJ, Faris M;

WPI; 2004-580991/56.

The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence witch encodes the composition that corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID No.3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that encodes the protein; (3) a composition comprising a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide content of the polymucleotide described above; (4) content is a full complement of the polymucleotide described above; (4) content is a full complement of the polymucleotide described above; (4) content is a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human composition that comprises the composition described above in a human composition that produces the antibody; (11) delivering a cytotoxic agent composition growth, reproduction or survival of cancer cells that expresses the protein of P1; (7) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1; (1) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1; and cell in gene therapy. The compositions welease the protein of P1; and cell in gene therapy. The compositions welease the protein of P1; and cells that expresses the protein of P1; and cells and detecting cancer. The present sequence represents a cell that expresses the protein of P1; and cell in the exemplification of the composition cells and dete ö Gaps 254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.5; chromosome 6. ö Length 29; 0; Indels 1.3%; Score 14; DB 8; Le 100.0%; Pred. No. 3.1e-05; tive 0; Mismatches 0; Human 254P1D6B v.5 peptide SEQ ID NO:268. ADR00857 standard; peptide; 29 AA. 23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P 143 FLGKDWGLEEMSEY 156 1 FLGKDWGLEEMSEY 14 04-NOV-2004 (first entry) Query Match 1.3 Best Local Similarity 100. Matches 14; Conservative (AGEN-) AGENSYS INC. WO2004067716-A2 Sequence 29 AA; Homo sapiens 12-AUG-2004. ADR00857; ADR00857 ID ADR( RESULT 5 g 8

Ge ₩;

Challita-Eid PM,

Jakobovits A,

Perez-Villar JJ, Faris M;

Raitano AB,

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The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or cleven contiguous amino acids of a protein of figure 2 [P1, see SEQ ID NO:3, 5 or 7 ADRO0592, ADRO0594 or ADRO0566), or a peptide included in that is at least 90, 91, 32, 93, 94, 95, 96, 97, 98, or 93% homologous or that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) constraint a mammalian immune response directed to the protein or a certatus of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition that modulates the composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and con be composition or survival of cancer cells that expresses the protein of P1; and con be useful of or treating and detecting cancer. The present exemplification of the human 254PID6B see the protein of P1 such the exemplification of the present invention. The human 254PID6B gene is located on chromosome 6p22.
s to the nucleic acid ORF sequence which encodes the 254PlD6B corresponds to a subsequence of the ORF, useful for detecting
                                                                                                          Example 13; SEQ ID NO 268; 345pp; English.
                                                      and treating cancer.
     corresponds to
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ô Gaps ; 0 DB 8; her. o. 3.1e-05; 0; Indels 1.3%; Score 14; DB 100.0%; Pred. No. 3.1 artive 0; Mismatches 128 GIWGDSPEDIRKDL 141 Query Match Best Local Similarity 100. Matches 14; Conservative Sequence 29 AA; 8

ADR00673 standard; peptide; 9 AA. 1 GIWGDSPEDIRKDL 14 RESULT 6 ADR00673 g

Human 254P1D6B peptide SEQ ID NO:84. (first entry) 04-NOV-2004 ADR00673;

254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human;

24-JAN-2003; 2003US-0442526P.

(AGEN-) AGENSYS INC

23-JAN-2004; 2004WO-US001965. WO2004067716-A2. chromosome 6. Homo sapiens. 12-AUG-2004 XBXBXBXBXSXEXEXBXBXBXBX

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The present introductions a 2347100 Small inteleting. The present interaction that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the curresponds to subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists of a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in comparison that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98 homologous or identical to an entire amino acid sequence of Pl; (2) a polynucleotide contact in a full complement of the polynucleotide described above; (4) composition composition that a protein or a 254PlD6B-related polynucleotide described above; (4) composition in that modulates the composition described above; (4) a cell that expresses a protein of Pl; (7) a pharmaceutical composition that modulates the composition that modulates the composition described above; (8) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that expresses the antibody; (10) a contract of agent to a distribute of a contract of agent or a distribute or a contract of agent or a distribute or a contract of agent or a distribute or a contract or agent the arrangement of a contract or a gent to a contract or a contract or a protein of Pl; (7) a pharmacoutical contract or a protein or a protein of Pl; (8) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that expresses the antibody; (10) a non-human transgenic animal that expresses the antibody; (10) a non-human transgenic animal that expresses the antibody; (10) a non-human transgenic animal that expresses the antibody; (10) a non-human transgenic animal that expresses the antibody; (10) a non-human transgenic animal that expresses the antibody; (10) a non-human tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or a diagnostic agent to a cell that expresses the protein of PI; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of PI. 254PLD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PLD6B peptide, which is used in the exemplification of the present invention. The human 254PLD6B gene is located on chromosome 6p22.
                                                                                                                                                        New 254PID6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PID6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a 254P1D6B small interfering RNA (siRNA)
                                                                                                                                                                                                                                                                                                                                                                   Example 9; SEQ ID NO 84; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
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0; Indels 0.8%; Score 9; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; Mismatches 0.50, 100.0%; FL ADR00720 standard; peptide; 9 AA. 9; Conservative 320 ELPISPTTA 328 σ ELPISPTTA Local Similarity ADR00720; Query Match Best Loca Matches RESULT 7 ADR00720 ઠ 엄

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Gaps

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254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; Human 254P1D6B peptide SEQ ID NO:131. chromosome 6.

(first entry)

04-NOV-2004

WO2004067716-A2. Homo sapiens

12-AUG-2004.

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composition that comprises a double stranded siRMA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PID68 protein, or corresponds to a subsequence of the ORF, where the double stranded siRMA is 19, 20, 21, 22, 23, 24, or 25 contiguous an length. Also described: (1) a composition that comprises, consists essentially of, or consists (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or deven contiguous amino acids of a protein of figure 2 (PI, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00556), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that encodes the protein; (3) a composition comprising a polymucleotide that is a full complement of the polymucleotide described above; (4) dencetting in a sample, the presence of a 254PID6B-related protein or a 254PID6B-related polymucleotide; (6) a composition that modulates the composition that comprises the composition described above; (10) a pharmaceutical composition that comprises the composition described above; (10) a not than transganic animal that produces the antibody; (10) a not than transganic animal that produces the antibody; (10) a not than transganic animal that produces the antibody; (10) a part of the composition that modulates and a non-human transganic animal that produces the antibody; (10) a part of the composition that modulates and a non-human transganic animal that produces the antibody; (10) a part of the composition that produces the antibody; (10) a part of the composition that the antibody or the fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybridoma that produces the antibody; (11) delivering a cytocoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 24P1D6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254P1D6B peptide, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on chromosome 6p22.
                                                                                                                                                                                 New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                    The present invention describes a 254P1D6B small interfering RNA (siRNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                     Ge ₩;
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                                                                                                   Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                   Example 9; SEQ ID NO 131; 345pp; English.
                                                                                                   Jakobovits A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 9; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.8%; Sco
Best Local Similarity 100.0%; Pr
Matches 9; Conservative 0;
23-JAN-2004; 2004WO-US001965.
                                 24-JAN-2003; 2003US-0442526P.
                                                                                                 Raitano AB, Ja
R JJ, Faris M;
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                                                                  (AGEN-) AGENSYS INC.
                                                                                                                                                  WPI; 2004-580991/56.
                                                                                                                                                                                                                                  treating cancer.
                                                                                                               Perez-Villar JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
                                                                                                   SB,
                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting

Example 9; SEQ ID NO 133; 345pp; English.

and treating cancer.

Ge ₩;

Jakobovits A, Challita-Eid PM,

Kanner SB, Raitano AB, Ja Perez-Villar JJ, Faris M;

(AGEN-) AGENSYS INC.

WPI; 2004-580991/56.

23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P.

WO2004067716-A2

12-AUG-2004

Homo sapiens.

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the composition that corresponds to a subsequence of the ORF, where the cube stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous cucleotides in length. Also described: [1] a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID ONC), 5 or 7 ABR00595, ABR00596, or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein can or of that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or dentical to an entire amino acid sequence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) detecting, in a sample, the presence of a 254P1D6B-related polymucleotide; (6) a composition that modulates the cappacition that comprises the composition described above in a human composition that the antibody or its fragment, which is monoclonal; (9) which shams that antibody or its fragment, which is monoclonal; controlled and antibody or its fragment, which is monoclonal; controlled and antibody or its fragment, which is monoclonal; controlled and antibody or its fragment, which is monoclonal; controlled and antibody or its fragment, which is monoclonal; controlled and antibody or its fragment and an antibody or a protein or a controlled and antibody or its fragment, which is monoclonal; controlled and antibody or its fragment, which is monoclonal; controlled and antibody or its fragment, which is monoclonal; controlled and antibody or its fragment, and an antibody or its fragment and an antibody or in a sequence of a controlled and antibody or interface or an antibody or an antibody or an antibody or an antibody or an antibody or an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or a diagnostic agent to a cell that expresses the protein of PI; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of PI. 254PLD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PLD6B peptide, which is used in the exemplification of the present invention. The human 254PLD6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hybridoma that produces the antibody; (11) delivering a cytotoxic agent
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100.0%; Pred. No. 1.8
Live 0; Mismatches
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les 9; Conserv
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254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human;

chromosome 6.

Human 254P1D6B peptide SEQ ID NO:133.

(first entry)

04-NOV-2004

ADR00722;

ADR00722 standard; peptide; 9 AA

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human;

Human 254P1D6B peptide SEQ ID NO:170.

04-NOV-2004 (first entry)

ADR00759;

ADR00759 standard; peptide; 9 AA.

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The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the corresponds to a subsequence of the ORF, where the capture stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 21, 22, 23, 24, or 25 contiguous concleted siRNA is 20, 21, 22, 21, 22, 23, 24, or 25, 21, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 23, 24, 22, 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                  254PID6B; small interfering RNA; siRNA; immune response;
254PID6B-related protein; cytostatic; gene therapy; cancer; human;
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100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0; Indel
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Human 254PlD6B peptide SEQ ID NO:157
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Best Local Similarity 100...
9, Conservative
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                                                                                                                                                                                                                           chromosome 6.
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting

Example 9; SEQ ID NO 170; 345pp; English.

and treating cancer.

Ge ₩;

Challita-Eid PM,

Perez-Villar JJ, Faris M;

WPI; 2004-580991/56.

(AGEN-) AGENSYS INC.

23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P

WO2004067716-A2

12-AUG-2004.

chromosome 6. Homo sapiens.

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The present invention describes a 254Plb6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the cast and open reading frame (ORF) sequence of the ORF, where the 254Plb6B protein, or corresponds to a subsequence of the ORF, where the couble stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists as essentially of, or consists of a peptide included in contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID CC onsists as essentially of, or consists of a protein of figure 2 (Pl, see SEQ ID CC onsists of peptides, or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein cthat is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that is at least 90, 91, 32, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) generating a mammalian immune response directed to the protein of a cell that expresses a protein of Pl; (7) a pharmaceutical composition that modulates the composition that modulates the composition that modulates the composition that produces the antibody or its fragment, which is monoclonal; or a non-human transgenic animal that expresses the protein of Pl; and correcting a call that expresses the protein of Pl; and correction or all that expresses the protein of Pl; and correction or all problems that produces the antibody; (10) a composition or survival of cancer cells that corpositions molecules and methods are useful correcting one therapy. The compositions, molecules and methods are useful contacting and an encoderance of the present sequence represents the protein of the present sequence represents the presents and encoderance of the present sequence response the presents and methods are useful contacting and an encodenced and encode encoderating canner.
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305 PTPPTSAAP 313

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Gaps

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47 RVSHTFPVV 1||||||||| 1 RVSHTFPVV

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RESULT 10 ADR00759

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PTPPTSAAP 9
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RESULT 11

ADR00767 standard; peptide; 9 AA. 8%CCCCCCCCCCCCCCCCCCCCCCCCCCX8%HHHHKK8%HLX8%HHHK8%X8%AMAMA

ADR00767;

(first entry) 04-NOV-2004

Human 254P1D6B peptide SEQ ID NO:178.

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; chromosome 6.

Homo sapiens

WO2004067716-A2.

12-AUG-2004.

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P.

(AGEN-) AGENSYS INC.

Ge W; Challita-Eid PM, Jakobovits A, Perez-Villar JJ, Faris M; Raitano AB,

WPI; 2004-580991/56.

New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 9; SEQ ID NO 178; 345pp; English.

The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID COOR); So T ARD00959, or a peptide included in any of the 42 lists of peptides of sequence of P1, (2) a polynucleotide that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) denerting a mammalian immune response directed to the protein of P1; (5) a generating in a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related protein or a 254P1D6B-related protein or a composition that modulates the composition that modulates the composition that comprises the composition described above; (4) a pharmaceutical computes of a composition that modulates the composition that comprises the composition and that composition and that comprises the composition and that comprises the composition described above in a human contract and a protein of a composition that modulates the composition that modulates the composition that modulates the composition that comprises the composition described above in a human contract and an antibody or its fragment, which is monoclonal; (9) which does form; (8) an antibody or its fragment, which is monoclonal; (9) a contraction or a contraction or a composition and an antibody or its fragment, which is monoclonal; (9) a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction or a contraction o or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P1D6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254P1D6B peptide, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on chromosome 6p22. hybridoma that produces the antibody; (11) delivering a cytotoxic agent

Sequence 9 AA;

The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the cash protein, or corresponds to a subsequence of the ORF, where the 254P1D6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID NO:3, 5 or 7 ADROGS2, ADROGS4 or ADROGS56), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein contiguous that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of a 254P1D6B-related protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition described above in a human cuntiled or shimman transgenic animal that produces the antibody; (10) a pnarmaceutical continual transgenic animal that produces the antibody; (10) a pnarmaceutical continual transgenic animal that produces the antibody; (10) a pnarmaceutical continual composition that modulates animal that produces the antibody; (10) a pnarmaceutical continual composition animal that produces the antibody; (10) a pnarmaceutical continual continual animal transgenic animal that produces the animal animal animal transgenic animal that produces the animal animal transgenic animal that produces the animal animal transgenic animal that produces the animal animal transgenic animal that produces the animal animal animal transferince animal that produces the animal animal animal transferince animal that produces the animal animal animal animal animal animal animal animal animal animal New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cytostatic activity, and can be Gaps 254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; Ge ₩; ö Kanner SB, Raitano AB, Jakobovits A, Challita-Eid PM, Perez-Villar JJ, Paris M; 0; Indels Length 9; DB 8; Le: 0.8%; Score 9; DB 8 100.0%; Pred. No. 1.8 tive 0; Mismatches Example 9; SEQ ID NO 208; 345pp; English. Human 254P1D6B peptide SEQ ID NO:208. ADR00797 standard; peptide; 9 AA. 23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P. 04-NOV-2004 (first entry) Query Match
Best Local Similarity 100...
Local Similarity 100... 363 PVETTYNYE 371 (AGEN-) AGENSYS INC. and treating cancer. WPI; 2004-580991/56. 1 PVETTYNYE WO2004067716-A2 chromosome 6. Homo sapiens. 12-AUG-2004. ADR00797; RESULT 12 ADR00797 ઠે 유

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The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the couble stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous couble stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of Pl; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein or a catture of a smple, the presence of a 254PlD6B-related protein or a catture of a composition that modulates the catture of a cell that expresses a protein of Pl; (7) a pharmaceutical composition that composition described above in a human
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used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254P1D6B peptide, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on chromosome 6p22.
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                                                                                                                                                              Gaps
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254PID6B-related protein; cytostatic; gene therapy; cancer; human;
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human 254P1D6B peptide SEQ ID NO:210.
                                                                                                                                                                                                                                                                                                                              ADR00799 standard; peptide; 9 AA.
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Perez-Villar JJ, Faris
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                                                                                        Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 6.
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composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254P106B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 4, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADRO0592, ADRO0594 or ADRO0596, or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 31, 92, 33, 94, 95, 96, 97, 98, or 99* homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide
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unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a coll that expresses the protein of Pi; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of Pi 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
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254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 254PlD6B peptide SEQ ID NO:246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR00835 standard; peptide; 9 AA.
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                                                                                                                                                                                                                     Sequence 9 AA;
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that is a full complement of the polynucleotide described above; (4)
generating a mammalian immune response directed to the protein of Pl; (5)
detecting, in a sample, the presence of a 254PloBe-related protein or a
C254PloBe-related polynucleotide; (6) a composition that modulates the
status of a cell that expresses a protein of Pl; (7) a pharmaccutical
composition that comprises the composition described above in a human
unit dose form; (8) an antibody or its fragment, which is monoclonal; (9)
a non-human transgenic animal that produces the antibody; (10) a
a non-human transgenic animal that produces the antibody; (10) a
cor a diagnostic agent to a cell that expresses the protein of Pl; and
c12) inhibiting growth, reproduction or survival of cancer cells that
express the protein of Pl. 254PlD6B has cytostatic activity, and can be
used in gene therapy. The compositions, molecules and methods are useful
cor treating and detecting cancer. The present sequence represents the
human 254PlD6B peptide, which is used in the exemplification of the
present invention. The human 254PlD6B gene is located on chromosome 6p22.
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; 0; Indels 0.8%; Score 9; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; iive 0; Mismatches 0; Indel Best Local Similarity 100. Matches 9; Conservative 558 QIVLYEWSL 566 σ 1 QIVLYEWSL Query Match ð

Gaps

ADR00645 standard; peptide; 9 AA. RESULT 15 ADR00645

Human 254PlD6B peptide SEQ ID NO:56. (first entry) 04-NOV-2004 ADR00645; 

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; chromosome 6.

Homo sapiens.

WO2004067716-A2.

12-AUG-2004.

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P.

(AGEN-) AGENSYS INC.

New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer. Kanner SB, Raitano AB, J Perez-Villar JJ, Faris M; WPI; 2004-580991/56.

Jakobovits A, Challita-Eid PM,

Example 9; SEQ ID NO 56; 345pp; English.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to 254PID6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or

cc eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID N0:3, 5 or 7 ADR00592, ADR00594 or ADR00596, or a peptide included in cany of the 42 lists of peptides, given in the specification, or a protein c that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 93% homologous or identical to an entire amino acid sequence of P1; (2) a polymucleotide control that encodes the protein; (3) a composition comprising a polymucleotide c that is a full complement of the polymucleotide described above; (4) c generating a mammalian immune response directed to the protein of P1; (5) generating a mammalian immune response directed to the protein of P1; (5) c generating in a sample, the presence of a 254PD6B-related protein or a 254PD6B-related polymucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and can be composition or survival of cancer cells that expresses the protein of P1; 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B gene is located on chromosome 6p22. \$

0.8%; Score 9; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0; Indela Query Match 0.8 Best Local Similarity 100. Matches 9; Conservative 129 IWGDSPEDI 137 ઠે

Sequence 9 AA;

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Sequence 261, App
Sequence 261, App
Sequence 43, Appl
Sequence 266, App
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Sequence 266, App
Sequence 266, App
Sequence 265, App
Sequence 1184, App
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2. (cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
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7. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
8. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
9. (cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
11. (cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
12. (cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
13. (cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
14. (cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
15. (cgn2_6/ptodata/2/pubpaa/USIO8_PUBCOMB.ppp:*
16. (cgn2_6/ptodata/2/pubpaa/USIO8_PUBCOMB.ppp:*
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18. (cgn2_6/ptodata/2/pubpaa/USIO8_PUBCOMB.ppp:*
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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length: 35
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411, Appl
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US-09-769-180-3
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US-10-764-390-131
US-10-764-390-131
US-10-764-390-131
US-10-764-390-249
US-09-984-130-64
US-09-984-130-64
US-10-764-390-240
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US-10-764-390-56
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## ALIGNMENTS

```
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REPERENCE: 51168-20081.00
CURRENT FILING DATE: 2004-01-23
FRIOR PILING DATE: 2004-01-23
FRIOR PILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 268
LENGTH: 29
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Pred. No. 0.0062;
0; Mismatches 1; Indels
Sequence 268, Application US/10764390 Publication No. US20040214212A1 GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
                                                                                                         Raitano, Arthur B.
Jakobovits, Aya
Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.8%;
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Best Local Similarity 96.6
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-764-390-268
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128 GIWGDSPEDIRKDLXFLGKDWGLEEMSEY 156

Gaps

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Indels

0; Mismatches

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18; Conservative
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ORGANISM: Homo sapiens
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US-10-764-390-43
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LENGTH: 16
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US-10-764-390-262

US-10-764-390-262

Sequence 262, Application US/10764390

Publication No. US20040214212A1

GENERAL INFORMATION:

APPLICANT: Railano, Arthur B.

APPLICANT: Railano, Arthur B.

APPLICANT: Ge, Wangmao

APPLICANT: Ge, Wangmao

APPLICANT: Ge, Wangmao

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

TITLE OF INVENTION: Butiled 254P1D6B Useful in Treatment and Detection of

TITLE OF INVENTION: Butiled 254P1D6B Useful in Treatment and Detection of

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

FILE REFERENCE: 51158-20081.00

CURRENT APPLICATION NUMBER: US/10/764,390

CURRENT APPLICATION NUMBER: US/04-01-23

PRIOR PILING DATE: 2004-01-24

NUMBER OF SEQ ID NOS: 277

SEQ ID NO 262

LENGTH: 29

LENGTH: 29
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APPLICANT: Raitano, Arthur B.
APPLICANT: Takboovits, Aya
APPLICANT: Takboovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Tanner
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Steven B. Kanner
FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION WUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US/0/442,526
PRIOR APPLICATION NUMBER: 2003-01-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 101; DB 16; Length 19; 94.7%; Pred. No. 11;
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1 FLGKDWGLEEMSEYADDYRELEKDLLQPS 29
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 261
LENCTH: 19
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Publication No. US20040214212A1
GENERAL INFORMATION:
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Best Local Similarity 96.69
Warches 28; Conservative
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CRGANISM: Homo sapiens
US-10-764-390-261
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US-10-764-390-262
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Best Local Similarity
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US-10-764-390-261
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Banesys, Inc.
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
ITILE OF INVENTION: Nucleic Acids and Corresponding Proteins
ITILE OF INVENTION: Nucleic Acids and Corresponding Proteins
ITILE OF INVENTION: Cancer
FILE REFERENCE: 51159-20081.00
CURRENT PRILING DATE: 2004-01-23
PRIOR PILING DATE: 2004-01-23
PRIOR PLILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARR: FastSEQ for Windows Version 4.0
SSPTWARR: FastSEQ for Windows Version 4.0
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Tallita-Eid, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Cancer
TITLE OF INVENTION: Entitled 254Plb6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
CURRENT FILING DATE: 2004-01-23
PRIOR PELLORICATION NUMBER: US60/442,526
PRIOR PRILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                           Sequence 267, Application US/10764390 Publication No. US20040214212A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43, Application US/10764390 Publication No. US20040214212A1 GENERAL INFORMATION:
148 WGLEEMSEYXDDYRELEKD 166
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CORGANISM: Homo sapiens
US-10-764-390-43
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APPLICANT: Raitano, Arthur B.
APPLICANT: Taitano, Arthur B.
APPLICANT: Taitano, Arthur B.
APPLICANT: Taitano, Arthur B.
APPLICANT: Challite-Eid, Pia M.
APPLICANT: Challite-Eid, Mangano
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Butitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: UNMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR PILING DATE: 2004-01-23
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: 00/540,217
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 52425
LENGTH: 19
                                                                                                                                 Score 84; DB 16; Length 17; Pred. No. 1.1e+02;
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; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-52425
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 52425, Application US/10450763; Publication No. US20050196754A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                         149 GLEEMSEYXDDYRELEK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAPPTGVLSSLLLLVTIA 18
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APPLICANT: Ratieno, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                        1 GLEEMSEYADDYRELEK 17
                                                                                                                                    Query Match 1.5%;
Best Local Similarity 94.1%;
Matches 16; Conservative (
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Best Local Similarity 100.
Matches 18; Conservative
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ORGANISM: Homo sapiens
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-390-260
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US-10-450-763-52425
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
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APPLICANT: Steven B. Kanne
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APPLICANT: Agains, Arthur B.
APPLICANT: Callita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT APPLICANTION NUMBER: US60/442,526
FRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
STEVEN CONTROL OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
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                                   Query Match 1.6%; Score 92; DB 16; Length 16; Best Local Similarity 100.0%; Pred. No. 31; Matches 16; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 94.1
Matches 16, Conservative
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ORGANISM: Homo sapiens
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SEQ ID NO 1
LENGTH: 34
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
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Publication No. US20020019016A1

FURBLICANT: Hulsteart, Frank

APPLICANT: Vanmechelen, Eugeen

APPLICANT: Vanderstichele, Huge

TITLE OF INVENTION: Differential Diagnosis of Neurological Diseases

FILE REFERENCE: INNS:027 (11362.0027.NPUS01)

CURRENT APPLICATION NUMBER: US/09/892.835

FRIOR APPLICATION NUMBER: US 09/892.835

PRIOR PILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: US 09/892.835

PRIOR PILING DATE: 2000-07-18

PRIOR PILING DATE: 2000-06-37

PRIOR APPLICATION NUMBER: EP 00870151.8

PRIOR PILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.2
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3.5e+02;
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1.4%; Score 79; DB
Best Local Similarity 100.0%; Pred. No. 3.5
Matches 14; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 138
LENGTH: 9
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Publication No. US20040214212A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
                                                                                                                                                                                                                                              11 CARKOCSEGRIYSN 24
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Matches 9; Conservative
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ORGANISM: Homo sapiens
                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-390-265
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  SEQ ID NO 265
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                       LENGTH: 24
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176 PRGSABYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVL 235
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APPLICANT: Vandechelen, Eugeen
APPLICANT: Vandechelen, Eugeen
TITLE OF INVENTION: Diagnosis of Tauopathies
FILE REFERENCE: US.112.T181
CURRENT APPLICATION NUMBER: US/09/769,180
CURRENT APPLICATION NUMBER: US/09/769,180
FRIOR APPLICATION NUMBER: EP 0087008.8
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/178,391
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ 1D NOS: 54
SOFTWARE: Patentin version 3.0
                                                                                                                                     NAME/KEY: MOD RES
1 LOCATION: (28)...(28)
2 OTHER INFORMATION: PHOSPHORYLATION THREONINE
US-09-892-835-1
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ORGANIEM: Artificial
PERTURE:
OTHER INFORMATION: Synthetic Peptide
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Publication No. US20040091942A1
GENERAL INFORMATION:
APPLICANT: VanMechelen, Eugeen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/09769180; Publication No. US20030194742A1; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-764-390-137
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovita, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
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APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Mucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT PILING DATE: 2004-01-23
FRIOR FILING DATE: 2003-01-24
FRIOR FILING DATE: 2003-01-24
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29.6%; Pred. No. 6.8e+03;
tive 6; Mismatches 7; Indels 37
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APPLICANT: Vanderstichele, Hugo
TITLE OF INVENTION: Diagnosis of Tauopathies
FILE REFERENCE: 11916.0016.DVUSO1 (INNSO16-1)
CURRENT APPLICATION NUMBER: US/10/682,103
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: 09/769,180
PRIOR APPLICATION NUMBER: EP 00870008.8
PRIOR APPLICATION NUMBER: EP 00870008.8
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VEREION 3.2
SEQ ID NO 3
LENGTH: 34
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SOFTWARE: FastSEQ for Windows Version 4.0
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1 LOCATION: (28)
2 OTHER INFORMATION: PHOSPHORYLATION
US-10-682-103-3
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; Sequence 41, Application US/10764390
; Publication No. US20040214212A1
; GENERAL INFORMATION:
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Best Local Similarity 29.69
Matches 21, Conservative
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Best Local Similarity 91.7
Matches 11, Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-60-767B-4

US-09-20-306B-19

US-08-602-999A-54

US-08-602-999A-54

US-09-901-124-54

US-09-938-315-54

US-09-430-564-15

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US-09-338-807-6

US-09-223-043-6

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US-08-280-047-10

US-08-388-10

US-08-389-11-2

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Maximum Match 100%
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Sequence 70, Appl
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APPLICANT: Vanderstichele, Huge
APPLICANT: Vanderstichele, Huge
APPLICANT: Vanderstichele, Huge
TITLE OF INVENTION: Differential Diagnosis of Neurological Diseases
FILE REFERENCE: INNS:027 (11362.0027.NPUSO1)
CURRENT APPLICATION NUMBER: US /09/892.835
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/218.907
PRIOR PILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: EP 00870151.8
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.2
LENGTH: 34
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US-09-910-009A-395
US-09-910-009A-413
US-09-910-009A-451
US-09-910-009A-451
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US-08-395-456C-4
US-08-395-456C-4
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US-08-395-356-34
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US-09-636-399A-15
US-09-636-399A-16
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LOCATION: (28)..(28)
OTHER INFORMATION: PHOSPHORYLATION THREONINE
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US-09-769-180-3
Sequence 3, Application US/09769180
; Patent No. 6680173
; GENERAL INFORMATION:
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; Sequence 1, Application US/09892835
; Patent No. 6670137
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Best Local Similarity 29.6'
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 LPLPTTPSSGE 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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          TYPE: PRT
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52:

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SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
                   INFORMATION FOR SEQ ID NO:
                                                                                                                     , MOLECULE TYPE: peptide US-08-658-136-52
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 PRGSAEYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61.5; DB 4;
Pred. No. 4.1e+02;
          APPLICANT: VanderElichele, Hugo
TITLE OF INVENTION: Diagnosis of Tauopathies
FILE REPERENCE: US.112.7181
CURRENT APPLICATION: UNBER: US/09/769,180
CURRENT FILING DATE: 2001-01-24
PRIOR PELICATION NUMBER: EP 00870008.8
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PACHICIN VERSION 3.0
SEQ ID NO 3
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.1%; Score 61.5; D
Best Local Similarity 29.6%; Pred. No. 4.1e
Matches 21; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: LASSEN, ELIZABETH
RECISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELECHOME: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52, Application US/08658136 Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: GENZYME CORPORATION ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD RES
LOCATION: (28)
COTHER INFORMATION: PHOSPHORYLATION
US-09-769-180-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMINGHAM

MASSACHUSETTS

TY: USA
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                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE:
APPLICANT: VanMechelen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-658-136-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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US-09-060-767B-4
; Sequence 4, Application US/09060767B
; Sequence 70-2015-2
; GENERAL INFORMATION:
; APPLICANT: Well, Gary
APPLICANT: Chandrashekar, Ramaswamy
; TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                           Gaps
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Query Match 1.1%; Score 59.5; DB 3; Length 35; Best Local Similarity 35.0%; Pred. No. 6.2e+02; Matches 14; Conservative 3; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 55; DB 4; Length 32; 45.2%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                   1 VAYHWDFGDGSPG----QDTDEPRAEHSYLRPGDYRVQV 35
                                                                                                                                           560 VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: 32 Human Secreted Proteins
FILE REPRENCE: PSOOGE1
CURRENT APPLICATION: 32 Human Secreted Proteins
FILE REPRENCE: PSOOGE1
CURRENT APPLICATION NUMBER: US/09/690,454
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: 09/189,144
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: May 30, 1997
PRIOR PELICATION NUMBER: 60/048,190
PRIOR PELLING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR FILING DATE: AUGUST 29, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                             US-09-690-454-177
; Sequence 177, Application US/09690454
; Patent No. 6531447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OUTLIAN, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: TIDER, James B.
ITILE OF INVENTION: S13 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennic -
STPPPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hassan, Helle
APPLICANT: Hassan, Henrik
APPLICANT: Clausen, Henrik
APPLICANT: Bennett, Eric P.
TITLE OF INVENTION: Glycosylation Using GalNAc-T4 Transferase
FILE REFERENCE: 8850*1
CURRENT APPLICATION NUMBER: US/09/217,306B
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.0%; Score 53.5; DB 4; Length 24; Best Local Similarity 50.0%; Pred. No. 1e+03; Matches 11; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                             Query Match 1.0%; Score 54; DB 4; Length 25; Best Local Similarity 45.8%; Pred. No. 9.8e+02; Matches 11; Conservative 2; Mismatches 11; Indels
TITLE OF INVENTION: H. capsulatum FILE REFERENCE: BJCH 9986 CURRENT APPLICATION NUMBER: US/09/060,767B CURRENT FILING DATE: 1998-04-15 PRIOR APPLICATION NUMBER: 60/043,332 PRIOR FILING DATE: 1997-04-15 NUMBER OF SEQ ID NOS: 9 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Caldocellum saccharolyticum
US-09-060-767B-4
                                                                                                                                                                                                                                                                                                                                                                                                                              291 PVLTVTPGSTEHSIPTPPTSAAPS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PTSTVTPTPTPTPTPTVTATPT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 TPGSTEHSIPTPPTSAAPSEST 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09217306B; Patent No. 6465220; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TPSAT---TPAPPSSSAPPETT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE
OTHER INFORMATION: Muc7
US-09-217-306B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-217-306B-19
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                                                                                                                                                                                     SEQ ID NO 4
LENGTH: 25
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LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
COUNTRY: New York
COUNTRY: U.S.A.
ZITH: New York
COUNTRY: U.S.A.
ZUE: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLAF COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: A13-5
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leblie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 1101-202
TELEFHONE: (212) 790-9090
TELEFROME (212) 790-9041/8864
TELEFRA: (212) 780-9741/8864
TELEFRA: (212) 869-9741/8864
TELEFRA: GA14 PERNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 3; 3 Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4980-007-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERRING/DOCKET NUMBER: 4980-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54, Application US/08278865
Patent No. 6303574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 SESTPSELPISPTTAP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.9%;
Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 SRSTPRPLPMLPTTRP 29
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        / MOLECULE TYPE: peptide
US-08-602-999A-54
                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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RESULT 10
US-09-938-315-54
; Sequence 54, Application US/09938315
; Patent No. 6703482
; GENERAL INFORMATION:
. APPLICANT: KAY, BRIAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 SESTPSELPISPTTAP 329
                                  314 SESTPSELPISPITAP 329
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                                                                                                      14 SRSTPRPLPMLPTTRP 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
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0.9%; Score 51; DB 3; Length 31;
Best Local Similarity 62.5%; Pred. No. 2.4e+03;
Matches 10; Conservative 1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: OULLIAM, Lawrence A.
APPLICANT: POWLKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: 1SOLATING AND USING SAME
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 54, Application US/09500124 Patent No. 6432920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 SESTPSELPISPITAP 329
(703) 413-3000
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REGISTRATION NUMBER: 18,
                      TELEFAX: (703) 411-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467
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LENGTH: 31 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                  TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-278-865-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-09-500-124-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                               amino acid
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TELEPHONE:
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APPLICANT: KAY, BRIAN K.
SPARKS, ANDREW B.
THORN, JUDITH M.
OUILLIAM, LAWRENCE A.
DER, CHANNING J.
TITLE OF INVENTION: SIC SH3 BINDING PEPTIDES AND METHODS OF INUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                               STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRIT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,315

FILING DATE: 23-Aug-2001

CLASSIFICATION: CUNKNOWN>

ATTORNEY/AGRY INFORMATION:

NAME: Villacorta, Gilberto M.

REFERENCE/DOCKET NUMBER: 34,038

REFERENCE/DOCKET WIMBER: 4980-007-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-430-564-9
US-09-430-564-9
Sequence 9, Application US/09430564
Fatent No. 6372467
GENERAL INFORMATION:
APPLICANT: John Blenis
APPLICANT: Calvin J. Kuo
TITLE OF INVENTION:
TITLE OF INVENTION: PRASER AND PSESSER GENES, PROTEINS,
TITLE OF INVENTION: PRASER, PROBES, AND DETECTION METHODS
FILE REFERENCE: 00246/506002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 54: US-09-938-315-54
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us-10-764-390-3.szlm35.rai

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US-09-223-043-6

| Sequence 6, Application US/09223043
| Patent No. 6177256
| GENERAL INFORMATION:
| APPLICANT: MCKenzie, Ian F.C.
| APPLICANT: Apostolopoulos, Vaso
| APPLICANT: Pieters, Geoff A.
| TITLE OF INVENTION: ANTIGENIC CARBOHYDRATE COMPOUNDS AND
| TITLE OF INVENTION: ANTIGENIC CARBOHYDRATE COMPOUNDS AND
| TITLE OF INVENTION: ANTIGENIC CARBOHYDRATE COMPOUNDS AND
| TITLE OF INVENTION: ANTIGENIC CARBOHYDRAPY
| NUMBER OF SEQUENCES: 1
| CORRESPONDENCE ADDRESS: ADDRESS: Dann Dorfman Herrell and Skillman STREET: Suite 720, 1601 Market Street
| CITY: Philadelphia STREET: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 2; Length 23;
Pred. No. 2.2e+03;
4; Mismatches 9; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/223,043
                                                                                                                                      FILING DATE:
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNUABER: 108 08/340,711
FILING DATE: 16-NOV-1994
APPLICATION NUMBER: AU PM323
FILING DATE: 24-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET VUMBER: 530547/PAS/WKR
TELECOMMUNICATION:
TELEPHONE: (215)563-4100
TELEPHONE: (215)563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 530547/PAS/MKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 TVTPGSTEHSIPTPPTSAPSE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: AU PM3223
FILING DATE: 24-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.9%;
Best Local Similarity 40.9%;
Matches 9; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (215,500
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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Patent No. 598552

GENERAL INFORMATION:
APPLICANT: McKenzie, Ian F.C.
APPLICANT: Apostologoulos, Vasso
APPLICANT: Pietersz, Geoff A.
TITLE OF INVENTION: THEIR USE IN IMMUNOTHERAPY
NUMBER OF SEQUENCES: 14

CORRESPONDENCES: Dann Dorfman Herrell and Skillman
STREET: Suite 720, 1601 Market Street
COTTY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 15, Application US/09430564
| Sequence 15, Application US/09430564
| Patent No. 6372677
| GENERAL INFORMATION:
| APPLICANT: Kay K. Lee-Fruman
| APPLICANT: Calvin J. Kuo Pessek Genes, PROTEINS,
| TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
| TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
| CURRENT FILING DATE: 1999-10-29
| CURRENT FILING DATE: 1999-10-29
| PRIOR PILING DATE: 1999-10-29
| WUMBER OF SEQ ID NOS: 16
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                         0.9%; Score 49; DB 3; Length 22; illarity 47.6%; Pred. No. 2e+03; Conservative 1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.9%; Score 49; DB 3; Length 22; Best Local Similarity 47.6%; Pred. No. 2e+03; Matches 10; Conservative 1; Mismatches 10; Indels
  CURRENT APPLICATION NUMBER: US/09/430,564
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,141
PRIOR FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
ESEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Pennsylvania
COUNTRY: United States of America
COUNTRY: 19103-2307.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ORGANISM: Homo sapiens
US-09-430-564-15
                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-564-9
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Best Local Similarity
Matches 10; Conserva
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LENGTH: 22
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; Sequence 6, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
    APPLICANT: McKenzie, lan F.C.
    APPLICANT: Apostolopoulos, Vasso
    APPLICANT: Pietersz, Geoff Allan
    TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
    TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
    TITLE OF INVENTION: Use in Immunotherapy
    FILE REFERENCE: 2368-McKenzie
    CURRENT FILING DATE: 2000-06-14
    PRIOR APPLICATION NUMBER: 09/223,043
    PRIOR FILING DATE: 1999-12-30
    NUMBER OF SEQ ID NOS: 69
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 6
    LENGTH: 23
    TYPE: PRT
    ORGANISM: Homo sapiens
    US-09-593-870A-6
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; TELECOMMUNICATION INFORMATION:
; TELEPAX: (215)563-4100
; TELEPAX: (215)563-4100
; TELEPAX: (215)563-4100
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acids
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US-09-593-870A-6
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Search completed: October 12, 2005, 10:31:46 Job time: 27 secs

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October 12, 2005, 10:25:25 ; Search time 67 Seconds (without alignments) 8193.267 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on:

US-10-764-390-3 5580 Title: Perfect score: Sequence:

1 MAPPIGVLSSLLLLVTIAGC.....VSMNGSIRNGASFSYCSKDR 1072

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

37082 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 35

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Q7m4e6 drosophila			P61104 ornithocton	P01535 anemonia su	Q61d14 homo sapien	Q8wlr1 homo sapien			Q6wy52 bacteriopha	P05912 simian immu	Q70222 human immun	Q9ymb1 human immun					bacill	Q80586 human immun	Q8j3x2 human immun	P01498 androctonus	Q8ixg1 homo sapien		Q74en3 geobacter s			-	9	-	Q9zg81 chlamydia t	Q83333 murine hepa
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H N N N N N N N N N N N N N		NARY; rel. 26, rel. 26, ion facto ster (Fru Arthropo Arthropo hilidae; a J.M.; tion fact tion fact cta 1261: .32	do do
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
PPMIG protein.
PPMIG protein.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 34 AA. PRT; STEQGRPEPPTSAAAS 28 PRELIMINARY; 13 Q6PJK3 Q6PJK3; RESULT 2 QEPJK3 g

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE=Brain,

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RAARARA RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR RAARAR R

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05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 45, Last annotation update)
Huwentoxin-V (HWTx-V) [Contains: Mutant of huwentoxin-V (mHWTx-V)].
Orntiboctomus huwena (Chinese bird spider) (Selenocosmia huwena).
Elukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Ornithoctonus.
                                                                                                                                                                                                                                                                                                                               Zhang P.-F., Chen P., Hu W.-J., Liang S.-P.; and a novel insecticidal peptide toxin from the spider "Huwentoxian", a novel insecticidal peptide toxin: indicates Selencoemia huwena, and a natural mutant of the toxin: indicates key amino acid residues related to the biological activity.";
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                                                                                                                                                                                                                                                     SEQUENCE, DISULFIDE BONDS, AND MASS SPECTROMETRY.
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.B., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.;
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DOI=10.1128/JB.184.16.4601-4611.2002;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D.;
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                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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EMBL; AE013624; AAM83835.1; -.
Hypothetical protein.
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Toxicon 42:15-20(2003).

-I-FUNCTION: MaTx-V reversibly paralyzes locusts and cockroaches, and causes death with larger doses. It has no effect on mice by intra-abdominal, nor intracerbroventicular injection. Its natural mutant mHwTx-V shows no effect on locusts, cockroachs, and mice.
-I-SUBCELJULAR LOCATION: Secreted.
-I-TISSUS SPECIFICITY: Expressed by the venom gland.
-I-MASS SPECIFICITY: MW=4111.4; MW=RR=0.4; METHOD=MALDI; RANGE=1-35; NOTE=FEF.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                        -!- MASS SPECTROMETRY: MW=3877.1; MW_ERR=0.4; METHOD=MALDI; RANGE=1-
                                                                                                                                                                                                           33; NOTE=Ref.1.
-!- MISCELLANEOUS: ED(50) of HwTx-V is 16 +/- 5 mg/kg to locusts. Direct protein sequencing; Neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-Chidoblast;
MEDLINE=78084776; PubMed=23311; DOI=10.1016/0014-5793(77)80699-6;
Martinez G., Kopeyan C., Schweitz H., Lazdunski M.;
"Toxin III from Anemonia sulcata: primary structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JTL-1986 (Rel. 01, Created)
21-JTL-1986 (Rel. 01, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Neurotoxin III (Toxin ATX-III).
Anemonia sulcata (Snake-locks sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=78044787; PubMed=21843;
Beress L., Wunderer G., Wachter E.;
"Amino acid sequence of toxin III from Anemonia sulcata.";
Hoppe-Seyler's Z. Physiol. Chem. 358:985-988(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
                                                                                                                                                                                                                                                                                                              By similarity.
By similarity.
By similarity.
CC39F421571CA523 CRC64;
                                                                                                                                                                                                                                                                                             Mutant of huwentoxin-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                           . No. 4.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       917 CSGHGHCDPLTKRCICSHLWMENLIQRYIWDG 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 CSQDGDC----CKHLQCHSNYEWCVWDG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                          Huwentoxin-V.
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR.
MEDLINE=93343891; PubMed=8102051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nynantheae; Actiniidae; Anemonia.
                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         31.2%;
                                                                                                                                                                                                                                                                                                                                                                            4117 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 84:247-252(1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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35 AA.

PRT;

STANDARD;

ORNHU

TXHS ORNHU
ID TXHS ORN
AC P61104;

RESULT 4

21 AA.

PRT;

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PRELIMINARY;
  CCCCCSVQKR 18
                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                     Name=HLA-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCK1 TITCA
P83243;
                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
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Best Local S
                                                                                                                                                                                                                                                                                                     alleles."
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                                                                           OSWLR1;
                                                              Q8WLR1
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                                    RESULT 7
Q8WLR1
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                                                                                                                                                                                                   3D-structure, Cnidocyst, Direct protein sequencing,
Ionic channel inhibitor, Neurotoxin, Sodium channel inhibitor, Toxin.
                                                                                                                                                                                                                                                                                                                                          Gaps
Norton R.S., Cross K., Braach-Maksvytis V., Wachter E.; "IH-NMR study of the solution properties and secondary structure of neurotoxin III from the sea anemone Anemonia sulcata.";
                                                                                    Manoleras N., Norton R.S.; "Three-dimensional structure in solution of neurotoxin III from the sea anemone Anemonia sulcata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

TISSUB-Peripheral blood;
MEDLINE-95038742; PubMed=7951233;
Haire R.N., Ohta Y., Lewis J.E., Fu S.M., Kroisel P., Litman G.W.;
Hrix, a novel human tyrosine kinase expressed in T cells shares
sequence identity with Tec family kinases and maps to 4p12.";
Hum. Mol. Genet. 3:897-901(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                         7; Indels 13;
                                                                                                                        Biochemistry 33:11051-11061(1994).
-!- FUNCTION: Binds specifically to the sodium channel.
-!- SUBCELLULAR LOCATION: Secreted; cnidocyst.
-!- SUBILARITY: Belongs to the sea anemone short toxin family.
PIR; A9146; TZAZ3.
PDB; ANS; NMR; @=1-27.
                                                                                                                                                                                                                                                                                                               0.9%; Score 47.5; DB 1; Length 27; 28.1%; Pred. No. 3.6e+04; ive 3; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 2; Length 18; Pred. No. 2.2e+04; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases. EMBL, U07791, AAA19597.1; -. GO; GO:0016301; F:kinase activity, IEA.
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18 18 19 D954E7BB497625B1 CRC64;
                                                                                                                                                                                                                                                                                         AA4E261FFAF34A7A CRC64;
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                                                                                                                                                                                                                                                                CS -> SC (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                   60 ACCDLSSCDLAWWFEGRCYLVSCPHKENCEPK 91
                                                                                                                                                                                                                                                                                                                                                                                 2 SCCP-----CYWGGCPWGQNCYPE 20
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                                                                           PubMed=7727358;
                                      Biochem. J. 293:545-551(1993)
                                                                                                                                                                                                                                                                                        2938 MW;
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Best Local Similarity 70.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tyrosine kinase (Fragment)
                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Peripheral blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                        27 AA;
                                                               STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                Ionic channel
DISULFID
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NON TER
SEQUENCE
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STRUCTURE BY NWR.
PubMed=11790849; DOI=10.1110/ps.33402;
Wang I., Wu S.H., Chang H.K., Shieh R.C., Yu H.M., Chen C.;
"Solution structure of a K(+)-channel blocker from the scorpion Tityus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20565534; PubMed=11113450; DOI=10.1016/S0014-5793(00)02253-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Batista C.V.F., Gomez-Lagunas F., Lucas S., Possani L.D.; "Tcl, from Tityus cambridgei, is the first member of a new subfamily of scorpion toxin that blocks K(+)-channels."; FEBS Lett. 486:117-120(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chelicerata; Arachnida; Scorpiones;
                                                                                                                                                                                                                                                                                     Vargas-Alarcon G., Gomez-Casado B., Martinez-Laso J., Granados J.,
Laytisee Z., Alegre R., Arnaiz-Villona A.,
"Differences in intron 2 sequences between B*39061 and B*39062 in
Amerindians: comparison with those of B*3901, B*5101, and B*52012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cambridgei.";
Protein Sci. 11:390-400(2002).
-!- FUNCTION: Blocks reversibly Shaker B potassium channels. Also
displaces binding of noxiustoxin to mouse brain synaptosome
                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                TISSUE=Blood;
MEDLINE=97246738; PubMed=9089103; DOI=10.1007/s002510050227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- MASS SPECTROMETRY: MW=2446.4; METHOD=MALDI; RANGE=1-23;
                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelo
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AA; 1972 MW; 5941EC53ECF3A73D CRC64;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Major histocompatibility complex class I (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 2; I
Pred. No. 2.7e+04;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
2xin Tcl (Alpha-KTx 13.1).
Tityus cambridgei (Amazonian scorpion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukāryota, Metazoa, Arthropoda, Cheli.
Buthida, Buthoidea, Buthidae, Tityus.
                                                                                                                                                                                                                                                                                                                                                                                                Immunogenetics 45:436-439(1997).
EMBL; L77205; AAL40076.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 NRPPAALGGSGPDRDL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 NRPPVAV--AGPDKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
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Gaps

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Indels

Length 29;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Transcriptional regulator that acts by binding to the trans-activating responsive sequence (TAR) RNA element and activates transcription initiation and/or elongation from the LTR
                Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
"Experimented evolution yields hundreds of mutations in a functional voiral genome.";
J. Mol. Evol. 57:241-248(2003).
EMBL. AX26477; AAP34129.1;
EMBL. AX264777; AAP34075.1;
EMBL. AX264777; AAP34075.1;
EMBL. AAP364075.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=88122665; PubMed=2893293; DOI=10.1038/331619a0;
Kestlar H.W., Li Y., Naidu Y.M., Butler C.V., Ochs M.F., Jaenel G.,
King N.W., Daniel M.D., Desrosiers R.C.;
"Comparison of simian immunodeficiency virus isolates.";
Nature 331:619-622(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAT protein (Transactivating regulatory protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%; Score 46; DB 1; Length 32;
42.1%; Pred. No. 5.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simian immunodeficiency virus (Mm251 isolate) (SIV-MAC).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 AA; 3556 MW; 211547CBE6F4D817 CRC64;
                                                                                                                                                                    0.8%; Score 46; DB 2; Le.
ilarity 47.1%; Pred. No. 4.7e+04;
Conservative 3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Activator, AIDS, Nuclear protein, RNA-binding,
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 09, Last sequence update) (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          32 AA
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MEDLINE=22990536; PubMed=14629033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 PEKAKKETVEKAVATAPGL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 09, Created)
                                                                                                                                                                                                                                                     11 LLLLVTIAGCARKQCSE 27
                                                                                                                                                                                                                                                                                       5 Milliviveclalycsb 21
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                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1988 (
01-NOV-1988 (
05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                                                    TAT_SIVM2
ID TAT_SIVM2
AC P05912;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=TAT;
                                                                                                                                                                      Query Match
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ID Q70222
AC Q70222;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
            -!- SIMILARITY: Belongs to the short scorpion toxin family. Potassium channel inhibitor subfamily.
PDB; 1JLZ; NWR; A=1-23.
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                           Interaction with Ca(2+)-activated K(+)
                                                                GO; GO:0005576; C:extracellular; NAS.
GO; GO:0019876; E:potassium channel inhibitor activity; IDA.
GO; GO:0019835; P:cytodysis; IDA.
GO; GO:0009405; P:cytodysis; IDA.
Interpro; IPR001947; Scorpion toxins.
SPOSITE; PS01138; SCORP SHORT TOXIN; FALSE NEG.
3D-structure; Direct protein sequencing; Ionic channel inhibitor;
Neurotoxin; Potassium channel inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; DaDNA viruses, no RNA stage; Caudovirales; Podoviridae; T7-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.8%; Score 47; DB 1; Length 23; Best Local Similarity 45.0%; Pred. No. 3.1e+04; Matches 9; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h Similarity 56.2%; Pred. No. 3.6e+04; 9; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bendukidze N.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                             channels (Potential).
D59BFADBC9F31700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AA; 2337 MW; 2AAEA853EC8BD316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 913 CLLKCSGHGHCDPLTKRCIC 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRKKCKGSGKC--INGRCKC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ579377; CAE18166.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 NRPPVAVA--GPDKEL 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||| |: ||||: | 7 NRPPAALGSPGPDRDL 22
                                                                                                                                                                                                                                                                                                                              2454 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                              23 AA;
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Q6WY52
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RESULT 9 Q7YP58

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16; Indels

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10; Conservative
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                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Priapulus caudatus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=37621;
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       Matches
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                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95074931; PubMed=7527089;
Mammano F., Salvatori F., Ometto L., Panozzo M., Chieco-Bianchi L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arch. Virol. 144:29-43(1999).
Arch. Virol. 144:29-43(1999).
GO: William BaA75967.1; -.
GO: GO: 0016021; C: integral to membrane; IEA.
GO: GO: 0016021; C: integral to membrane; IEA.
GO: GO: 0019031; C: viral capaid; IEA.
GO: GO: 0010913; C: viral envelope; IEA.
GO: GO: 0010913; C: viral envelope; IEA.
InterPro: IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Relationship between the V3 loop and the phenotypes of human immunodeficiency virus type 1 (HIV-1) isolates from children immunodeficiency virus type 1 (HIV-1) isolates from children immunodeficiency virus type 1 (HIV-1) isolates from children immunodeficiency virus type 1 (HIV-1) isolates from children J. Virol. 69.82-92(1995).

REMBL; U10001; AAA64813.1; -...

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R InterPro; IPR007710; GP120.

R InterPro; IPR007110; IG-11ke.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 2; Length 34;
Pred. No. 5.8e+04;
5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 TLPDNEVELKAFVAPAPPVETTYNYEWNLISHPIDYQGEIKQGH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TRPNNNTRRSIHIGPGRAF-----YPTDIIGDIRQAH 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 AA; 3851 MW; BB88F3A44AAAE0EF CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein v3 loop region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                  Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676,
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 AA
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                                                                                                                                                                    Human immunodeficiency virus 1.
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3878 MW;
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Best Local Similarity 25.0%,
....hes 11; Conservative
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35 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           De Rossi A.;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Stelengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Nature 0:0-0(1999).

EMBL; AF144895; AAD40651.1; -
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005504; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000375; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_like.
PROSITE; PSC0071; HOMEOBOX.

DNA-binding; Homeobox; Nuclear protein.
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
346 TLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 2; Length 27;
Pred. No. 4.7e+04;
4; Mismatches 5; Indels
                                        2 TRPNNNTRKGVYIGPG------RAVFYATDIIGDIRQAH 34
                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Priapulida; Priapulidae; Priapulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER 27 27 27 SEQÜENCE 27 AA; 3280 MW; 321AE16A0529F351 CRC64;
                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 AA.
                                                                                                                                                  27 AA
                                                                                                                                                                                                                                                                  Engrailed homeodomain protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      829 LTEORKDTLVROLAVLLNVLDSDIKV 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LTEQRRQELAKDLA--LN--ESQIKI 27
                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%,
Local 13; Conservative
```

```
RA Carucci D.J.;

RT "Genome sequence and comparative analysis of the model rodent malaria

RT parasite Plasmandium yoelii yoelii.";

RL Mature 419:512-519(2002).

CC -!- CAUTION: The sequence shown here is derived from an EmBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is

CC PREDIAMINAPED Whole genome shotgun (WGS) entry which is

CC PREDIAMINAPED Whole genome shotgun (WGS) entry which is

CC PREDIAMINAPED WHOLE SHOWS 1; -.

KW Hypothetical protein.

FT NOW TER 1

SQ SEQUENCE 29 AA; 3752 MW; 3497968C69392CCB CRC64;

Query Match

Query Match

Ouery Match 6; Mismatches 10; Indels 0; Gaps 0;

Matches 9; Conservative 6; Mismatches 10; Indels 0;
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Search completed: October 12, 2005, 10:30:37 Job time : 69 secs

1

935 LWMENLIQRYIMDGESNCEWSIFYV 959 | . | . | . | . . | . | . | . | . . | . | . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . . | . .

8 8

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5.1.6
Compugen Ltd.
   GenCore version
Copyright (c) 1993 - 2005
```

OM protein - protein search, using sw model

; Search time 21 Seconds
(without alignments)
4911.637 Million cell updates/sec October 12, 2005, 10:26:00 Run on:

US-10-764-390-3 5580

1 MAPPIGVLSSLLLLVTIAGC.......VSMNGSIRNGASFSYCSKDR 1072 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

7756 Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues

DB seq length: 0 DB seq length: 35 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	translation initia	cenA protein (IgA1	POU homeodomain pr	toxin III - snake-	tubulin alpha chai	neurotoxín P2 - sc	isocitrate dehydro	metallothionein -	gene 1.5 protein -	hypothetical prote				hypothetical prote		E	rece	neural cell adhesi	gamma-crystallin -	major immunophilin	IS1/cat protein -	gurmarin - Gymnema	ATP synthase beta-	ribosomal protein		retinoic acid rece	chain C	pollen allergen Po	tyrosine 3-monooxy
SUMMARIES		! ! !																												
SUM	ID	5593	140692	B49111	TZAZ3	C56635	NTSRPM	\$58433	SMMR	Q1BP57	F95172	C83797	D84404	T29628	G97596	167427	S63483	D49829	G39690	S12965	C49480	IS3186	JX0200	A48186	808569	A44912	167428	PT0286	A60372	PN0583
	DB	2	~	~	-	~	Н	~	-	н	~	~	~	~	~	~	7	N	~	7	7	7	~	~	~	~	~	~	7	7
	Length	32	25	25	27	34	35	22	25	53	35	28	31	31	31	34	20	28	29	30	32	33	35	23	28	30	34	18	20	27
عبن	Query Match	0.9	6.0	0.9	6.0	0.8	0.8		0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7
	Score	. 72	50.5	49	47.5	44	44	42	41	41	41	40.5	40.5	40.5	ö	40.5	40	40	40	40	40	40	40	•	39.5	٥.	ď	39	39	39
	Result No.		~	٣	4	2	9	7	60	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical 3.1K chymotrypsin (BC 3 hypothetical prote	photosystem I 14.4 group I allergen A neurotoxin BmK 41- group I allergen P group I allergen P	aspartate transcar hemoglobin Alv hypothetical prote hypothetical prote V3 domain peptide	alpha-glucosidase capsid protein VP1 45/47K antigen - M
JS0676 A61529 B85840	PQ0672 BS8493 A59356 B58493 F58493	S51176 S01811 G84147 C82520 PC2297	S21240 PQ0545 A49237
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22 28 29	9 9 9 9 9 9	2 W W W W 7 O 4 4 R	15 17
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30 31 32	. # # # # # # # # # # # # # # # # # # #	8 6 4 4 4 8 6 0 1 2	44 44 62 44 72

## ALIGNMENTS

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CyAccession: S55937

Rithernandez, G.; Sierra, J.M.

Biochim. Biophys. Acta 1261, 427-431, 1995

A;Pitle: Translation initiation factor eIF-4E from Drosophila: cDNA sequence and express A;Pitcle: Translation initiation factor eIF-4E from Drosophila: cDNA sequence and express A;Pitcle: Translation initiation factor eIF-4E from Drosophila: cDNA sequence and express A;Pitcle: Translation initiation factor eIF-4E from Drosophila: cDNA sequence and express A;Pitcles: protein factor eIF-4E from Drosophila: cDNA sequence and express A;Pitcles: protein factor protein factor eigenvector factor eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector eigenvector ei
translation initiation factor eIF-4B - fruit fly (Drosophila melanogaster) (fragments)
C;Species: Drosophila melanogaster
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: FlyBase:FBgn0013947
C;Superfamily: translation initiation factor eIF-4E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 51; DB 2;
68.8%; Pred. No. 4e+03;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.9
Best Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: FlyBase:Eif4F
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299 STEHSIPTPPTSAAPS 314 13 STEQGRPEPPTSAAAS 28 g ઠે

cenA protein (IgAlh) - Cellulomonas fimi (fragment)
C;Species: Cellulomonas fimi
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 22-Oct-1999
C;Accession: I40692
E;Accession: I40692
E;Ancession: L40692
E;Ancession: L40692
A;Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren FEMS Microbiol. Lett. 92, 199-204, 1992
A;Fitle: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human IgA

A;Reference number: 140692 A;Accession: 140692 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

A;Residues: 1-25 <RES> A;Cross-references: EMBL:X65780; NID:g312035; PIDN:CAA46663.1; PID:g312036

Gaps 6 Query Match
0.9%; Score 50.5; DB 2; Length 25;
Best Local Similarity 48.1%; Pred. No. 3e+03;
Matches 13; Conservative 2; Mismatches 3; Indels

5

303 SIPTPPTSAAPSESTPSELPISPTTAP 329

6

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Gaps ö

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RiRosso, J.P.; Rochat, H.
Toxicon 23, 113-125, 1985
Tyritle: Characterization of ten proteins from the venom of the Moroccan scorpion Androc A; Reference number: A94318; MUID:85193276; PMID:3992595
A;Accession: A01758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isocitrate dehydrogenase (NAD) (EC 1.1.1.41) chain 2 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58433
R;Zeng, Y.; Weiss, C.; Yao, T.T.; Huang, J.; Siconolfi-Baez, L.; Hsu, P.; Rushbrook, J.1
B;Cchan, J. 310, 507-516, 1995
A;Title: Isocitrate dehydrogenase from bovine heart: primary structure of subunit 3/4.
A;Reference number: S58432; MUID:95382766; PMID:7654189
                                                                                                                                                  A;Note: sequence extracted from NCBI backbone (NCBIN:128392, NCBIP:128391)
C;Superfamily: tubulin
F;28/Anding site: polyglutamate (Glu) (covalent) #status predicted
F;33-34/Cleavage site: Glu-Tyr (tubulin-specific carboxypeptidase) #status predicted
F;33-34/Cross-link: peptide (Glu-Tyr) (by tubulin-tyrosine ligase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Androctonus mauretanicus mauretanicus
C;Date: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                Ouery Match 0.8%; Score 44; DB 2; Length 34; Best Local Similarity 32.0%; Pred. No. 1e+04; Matches 8; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: scorpion neurotoxin
C;Keywords: neurotoxin; venom
F;1-18,4-25,15-30,19-32/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 42; DB 2; Le 50.0%; Pred. No. 7.2e+03; ive 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Dred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurotoxin P2 - scorpion (Androctonus mauretanicus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 30.4%; Pred. No. 1.16
Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q7M3F1
C;Superfamily: 3-isopropylmalate dehydrogenase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 EEMSEYXDDYRELEKDLLQPSGKQE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 EDMAALEKDYEEVGVDSIEGEGEEE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               913 CLLKCSGHGHCDPLTKRCICSHL 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 CATCCGGRGKC--VGPQCLCNRI 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 1-35 <ROS>
A,Cross_references: UNIPROT:P01498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 PPVANAGPNHTITL 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 PPSAKYGARHTVTM 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <ZEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                 A, Accession: C56635
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-34 <COE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A01758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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C;Species: Jl-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 10-Jul-1998
C;Accession: C56635
R;Coe, I.R.; Munro, R.; Sherwood, N.M.
B,Coe, I.R.; Munro, R.; Sherwood, N.M.
A)Ms Seq. 3, 257-262, 199
A;Title: Isolation of different brain-specific isotypes of alpha-tubulins from chum salm A;Reference number: A56635; MUID:93208376; PMID:1296820
                                                                                                                                                                                C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: B9111
R:Das, G.; Herr, W.
J. Biol. Chem. 268, 25026-25032, 1993
A:Title: Enhanced activation of the human histone H2B promoter by an Oct-1 variant gener A;Reference number: A49111; MUID:94043371; PMID:8227066
A;Contents: NTera 2D1
A;Accession: B49111
A;Accession: B49111
A;Accession: B49111
A;Accession: activation of the human histone (NCBIP:139679)
A;Residues: 1-25 cDAS>
A;Note: sequence extracted from NCBI backbone (NCBIP:139679)
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C;Species: Anemonia sulcata (snake-locks sea anemone)
C;Species: Anemonia sulcata (snake-locks sea anemone)
C;Date: 30-Apr-1979 #sequence_revision 24-Sep.1981 #text_change 09-Jul-2004
C;Accession: A51446; A51674; A61798
R;Martinez, G.; Kopeyan, C.; Schweitz, H.; Lazdunski, M.
FRES Lett. 84, 247-252, 1977
A;Title: Toxin III from Anemonia sulcata: primary structure.
A;Reference number: A91446; MUD: 78084776; PMID: 23311
A;Accession: A5446
A;Molecule type: protein
A;Residues: 1-27 < MAR>
A;Residues: 1-27 < MAR>
A;Accession: G; Wachter, B.
Hoppe-Seyler's Z. Physiol. Chem. 358, 985-988, 1977
A;Title: Amino acid sequence of toxin III from Anemonia sulcata.
A;Reference number: A91674; MUID: 78044787; PMID: 21843
A;Accession: A91674
A;Molecule type: protein
A;Residues: 1-21, SC', 24-27 < C;Comment: Three disulfide bonds are present.
C;Superfamily: toxin III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.9%; Score 49; DB 2; Length 25; Best Local Similarity 34.5%; Pred. No. 3.6e+03; Matches 10; Conservative 5; Mismatches 10; Indels
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Best Local Similarity 28.1<sup>§</sup>
Matches 9; Conservative
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Cispecies: Streptococcus pneumoniae
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Cipate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
CiAccession: F95172
Rifettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Atitle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Retus preliminary
A;Retus preliminary
A;Residues: 1-35 cKUR>
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A;Experimental source: strain TIGR4
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
R;Takami, H:; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira.
Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9KDN2; GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB048
A;Experimental source: strain C-125
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C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 0.2Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84404
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Danniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Title: Genome sequence of Halobacterium species NRC-1.
hypothetical protein SP1481 [imported] - Streptococcus pneumoniae (strain TIGR4)
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Pred. No. 1.6e+04;
----hea 7; Indels
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Best Local Similarity 42.1%;
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                        metallothionein - cultivated mushroom
C;Species: Agaricus bisporus (cultivated mushroom)
C;Species: Agaricus bisporus (cultivated mushroom)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A03286
R;Munger, K.; Lerch, K.
Biochemistry 24, 6751-6756, 1985
A;Title: Copper metallothionein from the fungus Agaricus bisporus: chemical and spectros
A;Attle: Copper metallothionein from the fungus Agaricus bisporus: chemical and spectros
A;Accession: A03286
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A; Accession: D84404

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C;Species: Rattus provegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 167427
R;Lopes da Silva, S.; Van Horssen, A.M.; Chang, C.; Burbach, J.P.
Endocrinology 136, 2276-2283, 1995
A;Title: Expression of nuclear hormone receptors in the rat supraoptic nucleus.
A;Reference number: 153294; MUID:95237162; PMID:7720676
A;Accession: 167427
A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: mRMA
A;Molecule type: mRMA
A;Residues: 1.34 <RES
A;Cross-references: GB:S77806; NID:9998991; PIDN:AAB34076.1; PID:g998992
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                                                                                           retinoic acid receptor homolog - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
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                                      A;Molecule type: DNA
A;Residues: 1-31 <STO>
A;Cross-references: UNIPROT:Q9HWH1; GB:AE004437; NID:g10581935; PIDN:AAG20600.1; GSPDB:G
C;Genetics:
A;Gene: VNG2544H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q8U567; GB:AE007869; PIDN:AAK87728.1; PID:g15157093; GSPDB:G
C;Genetics:
A;Gene: AGR_C 3588
A;Map position: circular chromosome
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R;Johnson, D.; Gattung, S.
Bubmitted to the EMBL Data Library, November 1995
A;Reference number: 220655
A;Reference number: 220658
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-31 <JOH>
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A;Residues: 1-31 <JOH
A;Residues: 1
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C;Species: Cenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29628
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                                                                                                                                                                                                                                                                                                                   Score 40.5; DB 2; Length 31;
Pred. No. 1.4e+04;
8; Mismatches 4; Indels
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Best Local Similarity 32.6%;
Matches 14; Conservative 8
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A;Status: preliminary
A;Molecule type: DNA
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A;Status: preliminary
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Sequence 32456, A Sequence 1932, Ap Sequence 10204, A Sequence 10204, A Sequence 10204, A Sequence 16, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10933, A Sequence 10933, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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US-09-543-681A-5434 US-08-793-273C-4

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Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 8, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 10208, A Sequence 10208, A Sequence 11984, A Sequence 1378, Ap Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	Drosophila melanogaster	4; Length 183; 69; Indels 0; Gaps 0; SDGATNSTTAALIVNNAVDYPPVAN 532  :
2 US-08-790-912-4 3 US-08-658-136-5 2 US-08-460-475-2 4 US-09-479-467A-2 4 US-09-052-469-8 4 US-09-052-262-8 4 US-09-052-262-8 4 US-09-052-262-8 4 US-09-052-262-8 4 US-09-052-262-8 4 US-09-052-262-6 4 US-09-902-540-11984 6 US-09-902-540-11984 7 US-09-902-540-11984 7 US-09-902-540-11984 7 US-09-902-540-11984 7 US-09-918-918-78 7 US-08-918-918-78 7 US-08-918-918-78 7 US-08-918-918-78 7 US-08-918-918-78 7 US-08-918-78	ALIGNMENTS /09270767 cids and proteins of e: 7326-094 17 aster	BB 4; 86-27; 8 69; 8 VTDSDCA VTDSDCA SLGPGASE : TTCASDE           PVARAGE PVARAGE 
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28 1700 29 168 0.5 30 168 0.5 31 168 0.5 34 34 34 34 34 34 34 34 34 34 34 34 34	RESULT 1 US-09-270-767- Sequence 324 Patent No. 6 GENERAL INFO APPLICANT: TITLE OF IN FILE REPERE CURRENT FILE CURRENT FILE NUMBER OF S SEQ ID. NO 32- LENGTH: 18 TYPE: PRT CRANIE: CORMINE: CORP. CORRENT FILE CORRE	Query Match Best Local Similarity Matches 92; Conserve Oy 473 INGPFIEEKTS Oy 533 AGPNHTITLE Oy 533 AGPNHTITLE Oy 593 GDYFCLKVII Db 121 GMYTFVLKVII Oy 653 HGI 655 Db 121 GMYTFVLKVII Oy 653 HGI 655 Db 181 IGI 183 RESULT 2 IS-O9-902-540-9932 SEQUENCE 9932, Applicat FRESULT 2 SEQUENCE 9932, Applicat FRESULT 2 SEQUENCE 9932, Applicat FRESULT 2 APPLICANT: GOLdman, B APPLICANT: Hinkle, G) APPLICANT: Hinkle, G) APPLICANT: Hinkle, G) APPLICANT: Hinkle, G) APPLICANT: Hinkle, G) APPLICANT: HINKLE, G) APPLICANT: HINKLE, G) APPLICANT: HINKLE, G) APPLICANT: HINKLE, G) APPLICANT: HINKLE, G) APPLICANT: HINKLE, G) APPLICANT: HINKLE, G) APPLICANT: Slater, St APPLICANT: WIGGANG, B TITLE OF INVENTION: M FILE REFERENCE: 38-10

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                                                                                                                                                            Query Match 5.6%; Score 312; DB 4; Length 1300;
Best Local Similarity 23.9%; Pred. No. 1.5e-15;
Matches 184; Conservative 98; Mismatches 291; Indels 198;
                                                                                                                                                          Length 1300;
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9932
LENGTH: 1300
                                                                                                   TYPE: PRT
ORGANISM: Myxococcus xanthus
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 10719-61.13
FILE REFERENCE: 10719-61.13
FILE REFERENCE: 10719-02-12
FRIOR PILING DATE: 1999-02-13
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR FILING DATE: 1998-08-13
FRIOR FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 215.5; DB 4;
; Pred. No. 3.8e-08;
77; Mismatches 314;
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US-09-902-540-10204
; Sequence 10204, Application US/09902540
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Best Local Similarity 23.3%;
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ORGANISM: Candida albicans
US-09-248-796A-17307
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Matches 168;
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Sequence 17307, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:

US-09-248-796A-17307

us-10-764-390-3.rai

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SMEKAL INFORMING.
APPLICANT: Evans, Glen A.
APPLICANT: Djabali, Malek
APPLICANT: Selleri, Licia
APPLICANT: Parry, Pauline
TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
                                                                                                                                                                                                                                                                                                                                     SESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNE----VELKAFVAPAPPVETTYN 369
                                                                                                                                                                                                                                                                                                                                                                           -----DPADYQRFLQAF-AKRGAGMGAKAPDRDSMDHVGVVESFAAGNFIEVT-S 442
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                                               L-PERSVLL------PLPTT------PSSGEVLEKEKASQLQE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Misgand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFRENCE: 38-10(15849)B
CURRENT PAPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 13786
LENGTH: 1093
                                                                                                                      Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 372;
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: HIGHEN, Barry S.
APPLICANT: HIGHEN, Gregory J.
APPLICANT: Midgand, Roger C.
APPLICANT: Widgand, Roger C.
APPLICANT: Widgand, Roger C.
APPLICANT: Widgand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and UFILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
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                                                                                                                                                                                                                                                                                                                                                                             3.7%; Score 206.5; DB 4;
25.1%; Pred. No. 5.3e-08;
iive 58; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 SSENAFGEGFVNVTVKPARRVNLPPVAVVSPQ-----
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                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10204
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Matches 86; Conserv
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                                                                           3334 ASSSSVINVVSMQTTTTPTSSASVPGHVTLTNPRLLGTPDIGSISNLLIKASQQSLGIQD 3393
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APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Proctein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT FILING DATE: 2000-329

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/179,965

PRIOR FILING DATE: 2000-02-01
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; OTHER INFORMATION: Polypeptide Accession Number Q03164
US-09-538-092-1262
     512 TNSTTAALIVNNAVDYPPVANAG-PNH-TITLPQ---
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SOFTWARE: CuraPatSeqFormatter Version 0.9
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                                           CORRESPONDENCE ADDRESS:
ADDRESSEB: Pretty, Schroeder, Brueggemann & Clark STREET: 444 South Flower Street, Suite 2000 CITY: LOS Angeles STATE: California COUNTRY: USA ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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3.3%; Score 184.5; DB 3;
Best Local Similarity 20.2%; Pred. No. 0.00016;
Matches 181; Conservative 115; Mismatches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,376
PILING DATE: 13-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Relect, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9387
TELECHONE: (619)546-4337
TELECHONE: (619)546-9392
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: unknown
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MEDIUM TYPE: Floppy
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                 3117 İNTSVLGPMGGGLTLTTGLNPSLPTSQSLFPSASKGLLPMSHHQHLHSFPAATQSSFPPN 3176
                                                                                                                                             :| | : | | : | | 3132
3177 ISNPPSGLLIGVQPPPDPQLLVSESSQRT----DLSTTVATPSSGLKKRPISKLQTRKNK 3232
                                                                                                                                                                                                              3335 ASSSSVLNVVSMQTTTTPTSSASVPGHVTLTNPRLLGTPDIGSISNLLIKASQQSLGIQD 3394
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                                                                                                                                                                                                                                                                                                1284 NIIKRSKSSIMYFEPAPLLPQSVGGTAATAAGTSTISQDTSHLTSGSVS-----GL 3334
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                                                    TY-----NYEWNLISHPTDYQGEIKQGHKQTL------N 394
                                                                                                                                                                                        -----NLPPVAVVSPQ-LQELT---LPLTSALID-GSQSTDDTELVSYHWEEINGP 476
                                                                                                                                                                                                                                                               675 DKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNN 734
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                                                                                                                     LSQLSVGLYV------KKVTVSSENAFGEGFVNVTV------KPARRV----
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,067
FILING DATE: 07-070-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
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TITLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
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4370 La Jolla Village Drive, Suite 700
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Patent No. 5811518
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CITY: San Diego
STATE: California
COUNTRY: United Sta
ZIP: 92122
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951 NCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMDEQERMELR 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 SY--HWEEINGPF----IBEKTSVDSPVLRLSNLDPGNY-SFRLTV--TDSDGATNSTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
3.3%; Score 183.5; DB 2; Length 822;
Best Local Similarity 21.4%; Pred. No. 1.4e-05;
Matches 165; Conservative 90; Mismatches 260; Indels 257;
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PILING DATE: 30-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAMB: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REPERENCE/POCKET NUMBER: P-LJ 1682
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       LENGTH: 822 amino acide TYPE: amino acid
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951 NCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELR 1010
----TATATVVVHVKDVNEAP-----VFVPPSKVIEAQEGIS 446
                                                                                                                                     779 INLVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLV 838
                                                                                                                                                                                 501 --VKANNYEVMVLATDSGNPPTTGTGTL------LLTLTDINDHGPIPEPRQIIIC 548
                                                                                                                                                                                                                                  839 RQLAV--LLINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKE 896
                                                                                                                                                                                                                                                             897 KADFL---LFKVLRVDTAGCLLKCSGHGHCDPLT--KRCICS-HLWMENLIQRYIWDGES 950
                                                                         648 -----FILPILGAVLALLT---LLLALLLLVRKKR-----KVKEPLLLPEDD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,481
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: P-LJ 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08472481
Patent No. 5863804
GENERAL INFORMATION:
APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
UNDMER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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CITY: San Diego
STATE: California
COUNTRY: United States
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 822;
                                                            GENERAL INFORMATION:
APPLICANT: Ranscht, Barbara
ATILE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,068A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
3.3%; Score 183.5; DB 2;
Best Local Similarity 21.4%; Pred. No. 1.4e-05;
Matches 165; Conservative 90; Mismatches 260;
                                                                                                                                                                                    3: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 EVQRLTVTDLDVPNWPAWRATYHIVGGDDGDH-----
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APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-WAY-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-007-1990
ATTOMAKE: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31, 915
REFERENCE/DOCKET NUMBER: P-LJ 1683
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPROX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 Sequence 9, Application US/08474068A
Patent No. 5837525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 822 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                          California
United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                             CITY: San Diego
STATE: Californi
COUNTRY: United SIP: 92122
                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-474-068A-9
US-08-474-068A-9
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APPLICAN:
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Barr, Maureen M.
TITLE OF INVENTION:
BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
FILE REPERENCE:
18021-2901B
CURRENT APPLICATION NUMBER: US/09/479,467A
CURRENT FILING DATE: 2000-01-06
                                                                                                                                                                                                                                                                                                         STIEPSTSTVITSPSTSPVISTVISSSSSSTIVITPISTESISTSPSSTVITSTIAPSTS 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVA-NAGPNHTITLPQNSITLN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTSTASTSTSTSTTYQQ-----SSSTITSSPSSTTLSTSIPTTTTPEITSTLSSLPDN
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                                                                                                                                        FNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVL----
                                                                                                                                                                                                                                                                                   ASLELSSVTVEKSP----VLTVTPGSTEHSIPTPPTSAAPSESTPSELPISPTTAP---
                                                                    Length 2870;
                                                                                                       Indels
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                                                                                                     97; Mismatches 259;
                  Elegans Lov-1 sy582 deletion protein
                                                                    3.3%; Score 183.5; DB 19.4%; Pred. No. 0.00011
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-TSDSTTIDSSNST-----
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                                                                                                       Conservative
                                                                  Query Match
Best Local Similarity
Matches 147; Conserv
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APPLICANT: Ster
                    ; ORGANISM: C. E
US-09-479-467A-15
TYPE: PRT
ORGANISM: C.
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APPLICANT: Barr, Maureen M.
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE HOMOLOGS REQUIRED FOR MALE MATTLE OF INVENTION: BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
TITLE OF INVENTION: BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
TITLE OF INVENTION: BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
FILE REFERENCE: 18021-2901B
CURRENT APPLICATION NUMBER: 05/09/479, 467A
CURRENT FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 16
SSOFTWARE: PATENTIN Ver. 2.0
SSOFTWARE: PATENTIN Ver. 2.0
LENGTH: 2870
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 40;
                                                         ENAFGEGFVNVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDD----TEIV 466
                                                                                                                                        QNDNKPKFTQDTFRGS------VIEGVMPGTSVMQVTATDEDDAVNTYNGVV 245
                                                                                                                                                                           SY--HWEEINGPF----IEEKTSVDSPVLRLSNLDPGNY-SFRLTV--TDSDGATNSTT :516
                                                                                                                                                                                                 -----FTITTHPETNQ 379
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                                                                                                                                                                                                                                                                                                                                                                                                                             380 ---GVLTTKKGLDF-------EAQDQH--TLYVEVTNEAPFAVKLP------ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                684 LQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRS 743
                                    359 APAPPVETTYNYE----WNLISHPTDYQGEIK---QGHKQTLNLSQLSVGLYVFKVTVSS
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 257;
 260; Indels
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 90; Mismatches
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 Conservative
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US-09-479-467A-15
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                                                                                                                                                                                                       Indels 253;
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                                                                                                                                                                  Query Match
Best Local Similarity 19.4%; Pred. No. 0.00013;
Matches 147; Conservative 97; Mismatches 259:
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              60/115,127
                                                                                                        TYPE: PRT ORGANISM: C. Elegans Lov-1 protein
PRIOR APPLICATION NUMBER: 60/1
                            PRIOR FILING DATE: 1999-01-0
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 4
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                                                                                         LENGTH: 3178
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US-09-949-016-9270 ; Sequence 9270, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al.

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRANCE PRIOR WINDOWS VERSION 4.0
SEQ ID NO 9270
LENGTH 2254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 SHSLPPA-----SLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPSELPI 323
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                                                                                                                                                                                                                                                                                                                                                                                                                             3.3%; Score 183; DB 4; Length 2254;
20.8%; Pred. No. 8.2e-05;
iive 83; Mismatches 302; Indels 276;
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US-09-949-016-9270
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Sequence 30227, Application US/09252991A
Patent No. 6551785
GENERAL INFORMATION:
TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: WICLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABOUT 1999-02-18
FRICA RAPLICATION NUMBER: US 60/074,788
FRICA PAPLICATION NUMBER: US 60/094,190
FRICA PAPLICATION NUMBER: US 60/094,190
FRICA FILING DATE: 1998-07-27
SEQ ID NO 30227
LENGTH: 2736
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758 VPTVVGDRPDTNVPGDHVATVEVTYPDGTKDTVEVTVHVTPKPVPDKDKYDP----TGG-
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      678 IATVTGLQ----VGTYHFRLTVKDQQGLSSTSTLTVAV---
                                                                                                                                                                                                                                                        787 TFHLRVTDSQGASDTDTATVEVQPDP 812
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US-09-252-991A-30227
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APPLICANT: STALHAWMAR-CARLEWALM, Margaretha
APPLICANT: STALHAWMAR-CARLEWALM, Margaretha
APPLICANT: STALHAWMAR-CARLEWALM, Margaretha
APPLICANT: STALHAWMAR-CARLEWALM
TITLE OF INVENTION: PROTEIN RIB, A CELL SURFACE PROTEIN THAT CONFERS IMMUNITY TO MANY
TITLE OF INVENTION: OF THE GROUP B STREPTOCOCCCUS: PROCESS FOR PURIFICATION OF THE PR
FILE REFERENCE: 0552-0140P
CURRENT APPLICATION NUMBER: US/09/434,123A
CURRENT FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
1906 GLDPAHRYKLLLYGLHHGKRVGPISAVAITAGREETETETTAPTPPAPEPHLGELTVEEA 1965
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                                                                                                          Gaps
                                                           826 VG-----QLTEQRKDTLVRQLAV1LNVLDSDIKVQKIRAHSDLSTVIVFYVQS
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ORGANISM: Group B Streptococcus - Strain A909
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Patent No. 6586580
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Matches 167; Conservative
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1494	649	1553	708	1587	767	1631	820	1690		
GQVTADGSGNWSFTPG1PLPDGTVVNVVARSP 1494			SDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQG-LSSTSTLT 708		VAVKKENNSPPRARAGGRH	: :       : :       : :	768 DGSDHSVALQLINLVEGVYTFHLRVTDSQGASDTDT-ATVE-VQPDPRKSGLVEL 820	DGSGKWAPTPATPLANGT-V]	TLOVGVGQLT 830	TAEAGATVILTDGNGNP
1463	604	1495	650	1554	709	1588	768	1632	821	1691
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Search completed: October 12, 2005, 10:19:17 Job time : 62 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                Copyright
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- protein search, using sw model OM protein October 12, 2005, 10:00:24 Run on:

; Search time 52 Seconds (without alignments) 1983.546 Million cell updates/sec

US-10-764-390-3 5580

1 MAPPIGVLSSLLLLVTIAGC.....VSMNGSIRNGASFSYCSKDR 1072 Perfect score: Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* 4:64 PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	titin, cardiac mus	titin - rabbit (fr	cal	projectin - fruit	probable RTX famil	projectin - fruit	large repetitive p	chitinase VCA0027	hypothetical prote	C protein alpha an	hypothetical prote	titin - rabbit (fr		hypothetical prote	hypothetical prote	gastric mucin (clo	probable tenascin	hypothetical prote	probable peptidogl	large repetitive p	collagen alpha 1(V	P-cadherin precurs	protein unc-22 [im	twitchin [similari	hypothetical prote	hypothetical prote	trithorax homolog	hypothetical prote	hemicentin precurs
SUMMAKIES	ΙD	I38344	820901	F90696	S24600	B85547	T13931	AC1018	D82510	C64483	A46405	T34434	146521	E90696	A85547	AH2493	147141	T09070	T34513	AI1489	AD0835	A54849	IJMSCP	A88852	S57242	T27935	T33369	A44265	T20992	T43290
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de	Query Match	4.0	3.7	3.7	3.7	3.6	3.6	•	3.6	3.6	٠	3.5	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.2	3.2
	Score	225	208.5	208	205	203.5	202.5	201.5	200.5	200.5	195.5	195.5	192.5	190.5	190.5	190	188	188	187.5	187	187	186	184.5	183	183	183	182.5	181.5	179	179
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## ALIGNMENTS

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text change 09-Jul-2004
C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text change 09-Jul-2004
C;Accession: 1303445; $\overline{5}$20898; $20897; $20899; $63565; $37393
R;Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titlins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330; PMID:7569978
                                          N;Alternate names: connectin
N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
cardiac muscle [validated] - human
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A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB A,Molecule type: mRNA A;Residues: 1-26926 <IABI) 
A;Residues: 1-26926 <IABI) 
A;Residues: 1-26926 <IABI) 
A;Cresidues: 1-26926 
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A; Actual control of a cid sequence not shown
A; Status: nucleic acid sequence not shown
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A; Molecule type: mRNA
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A; Molecule type: mRNB
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A; Molecule type: mRNB
A; Molecule type: mRNB
A; Molecule type: molecular understanding of titin.
A; Reference number: S20897; MUID:92258380; PMID:1582406

A;Accession: S20898
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule: 13597-14200, 17,14202-14696 clAB2>
A;Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
A;Accession: S20897
A;Status: nucleic acid sequence not shown; translation not shown A;Residues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3> A;Cross-references: BMBL:X64699; NID:937190; PIDN:CAA45940.1; PID:937191 A;Accession: S20899 A; Molecule type: mRNA

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Rosiques: 'Pr, 22278-22431,'R', 22433-22448,'G', 22450-22453,'Q', 22455-22480,'TR', 22483-2
A;Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
B;Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.
A;Title: Genomic organization of M line titin and its tissue-specific expression in two A;Reference number: S63665; MUID:96177761; PMID:8604138

A;Status: nucleic acid sequence not shown

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A;Residues: 1-6805 <LAB>
A;Cross-references: UNIPROT:Q28733; EMBL:X64696
A;Cross-references: UNIPROT:Q28733; EMBL:X64696
A;Oross-the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Labeit, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U.;
Nature 345, 273-276, 1990
                                                                                                                                                                                                                                                                                                                                     14084 SNVT--KNTATVSWKRPVDDGGSEITGYHVERREKKSLRWVRAIKTPVSDLRCKVTGLQE 14141
                                                                                                                                                                                                                                       4201 YDGGLEITGYVVEHQKVGDEAWIKDTTGTALRITQFVVPDLQTKEKYNFRISAINDAGVG 14260
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                                                                                                         VSYLWIR---DGQSPAAGDVID----GSD---HSVALQ-----LTNLVEG-VYTFHLRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GN-YSFRLTVTD--SDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQS
                                                                                                                                                                                                                                                                                                                                                                                                       TDSSRQQSTAXVTVIVQPENNRPP----VAVAGPDKELIFPVESATLDGSSSSDD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OS--RPPFKVLKAAEVARNLHMRLSKEKADFLLPKVLRVDTAGCLLKCSGHGHCDPLTKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930 CICSHLWMENLIQRYIWDGESN---CEWSIFYVTVLAFTLIVLTGGFTWLCICCCKRQKR
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titin - rabbit (fragment)

titin - rabbit (fragment)

c)Species: Oryctolagus cuniculus (domestic rabbit)

c)Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_cha

c)Accession: S20901, 146520

A.Title: Towards a molecular understanding of titin.

A.Reference number: S20897; MUID:92258380; PMID:1582406

A.Reference number: S20897; MUID:92258380; PMID:1582406

A.Status: nucleic acid sequence not shown; translation not s
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A; Wolecule type: DNA
A; Reduce; 26729-26825 - KOLD.
A; Cross-references: EMBL:X92412; NID:g1236761
R; Gaucel, M.; Leonard, K.; Labett, S.
EMBO, J. 12, 3827-3844, 1993
A; Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differentiat A; Reference number: 83733; MUD:94008990; PMID:8404852
A; Reference number: 83733; MUD:94008990; PMID:8404852
A; Reference number: 86284-62626 - KGAD
A; Residues: 2681-2626 - KGAD
A; Reference number: R66736; PD8:11TT
A; Contents: annotation; conformation by (1)H-NWR, residues 5253-5341
B; Pfull, M.; Pastore, A.
Submitted to the Brookhaven Protein Data Bank, August 1996
A; Reference number: R66201; PD8:10TF
A; Contents: annotation; conformation by (1)H-NWR, residues 5253-5341
B; Pfull, M.; Pastore, A.
Submitted to the Brookhaven Protein Data Bank, August 1996
A; Reference number: R66201; PD8:10TF
A; Contents: annotation; conformation by (1)H-NWR, residues 5253-5341
C; Genetics:
A; Genes: GDB:17N
A; Consos-references: GDB:127867; OMIM:188840
A; Genes: GDB:17N
A; Consos-references: GDB:127867; OMIM:188840
A; Genes: GDB:17N
A; Consos-references: GDB:127867; OMIM:188840
A; Consos-references: GDB:127867; OMIM:188840
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A; Consos-references: GDB:127867; OMIM:188840
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A; Consos-references: GDB:17867; OMIM:188840
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A; Consos-references: GDB:17867; OMIM:188840
A; Consos-references: GDB:17867; OMIM:188840
A; Map position: 2431-2432
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A; Map position: 2431-2432
A; Map position: 2431-2
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,21900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,248
F;26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : || : :||: || 13921 KDIRPSDITQITSTPTSSMLTIKKATRKDAGEYIITATNPFGTKVEHVKVTVLDVPGPPG 13980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------KKTGGSPITGYHLEFKE-RNSLLMKRANKTPIRMRDFKVTGLTEGLEYFFR 13752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13802 YDGGHKLTGYIVEKRDLPSKSMMKANHVNVPECAFTVTDLVEGGKYEFRIRAKNTAG-AI 13860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13651 FRVSAENKYGVGEGLKSEPIVARHPFDVPDAPPPPNIVÖ----VRHDSVSLTWTDP--- 13702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 YLVSCPHKENC-EPKKWGPIRSYLTFVLRPVORPAQLLDYGDMMLNRGSPSGIWGDSPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 IRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SSVGDSPAVPAE--TQQDPELHYLNESASTPAPKLPE-----RSVLLPLPTTPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.0%; Score 225; DB 1; Length 26926;
Best Local Similarity 19.5%; Pred. No. 0.027;
Matches 254; Conservative 186; Mismatches 414; Indels 448; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        =
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oy 735SI  Db 1657 VKEI  Oy 780 NLVB  Oy 780 NLVB  in homology; prd Db 1711 NLEB	B 59; QY 865 TVIV BP 90 Db 1830 EITV RI 915	138 RESULT 3	LY 403	556 QY 310 1380 Db 2964 604 QY 360 1429 Db 3017	SP 1481 Db 3074 VINN SS 703 QY 447 LPLT SD 1536 Db 3129 VDLT 719 QY 776 PFIE NL 1596 Db 3189 SW 734 QY 526 DYPP VT 1656 Db 3242 ASDN
under: 146520; MUID:90238546520 446520 Islated from GB/EMBL/DDBJ os: mRNA 235-5250 <1A2> nnces: EMBL:X17329; NID:gl ititin; fibronectin type iscle	53; Indels 39 AWWFEGRCYLVS SRGDWVTALA	91 KKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIR	347 LPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYGGELKQGHKQTLNLSQLSVGLY  1178	RITOTDSDGATNST-TAALIVNNAVDYPPVANAGPNHT	605 SRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHG-   1430 AGPGRPSDASKAVYAQDPLYPPGPPAFPKYDTTRSSVSLSWGKPAYDGGSP   655 IVFY
A;Title: A;Refere A;Rocess A;Rolecu A;Residu A;Cross- C;Reyworn	Best Los Matches Qy Db	8 6 6 6 6 6 6 6 6	6 6 6 6 6	8 6 8 6	6 6 6 6 6 6 6

S G	735SITLDGSRSTDDQRIVSYLWIRDQSPAAGDVIDGSDHSVALQLT 779 
ò	780 NLVEG-VYTFHLRVTDSQGASDTDTATVEVQPDPR 813
qq	
ò	RK-DTLVRQLA
qq	1771 SDGGSRITGYV-VDFLITEENKWQRVMKSLSLQYSTKDLNEGKQYTFRVSAENENGEGTPS 1829
ò	865 TVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLL 902
qa	DLKDLPDLCYLAKEN
RESULT F90696	THE COLOR AND ADDRESS OF THE COLOR AND ADDRESS
nypornerical C;Species: Es C;Date: 18-Ju	protein Eugosaz (importea) - Escherichia Coli (Birain Ols):n), Budsitain Scherichia coli 11-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accessio R;Hayashi, gasawara,	ssion: F90696 hib, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. A., N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res A;Title A;Refer	j. 8, 11-22, 2001 s: Complete genome sequence of enterohemorrhagic Bscherichia coli 0157:H7 and geno tence number: A99629, WUID:21156211, PMID:11258796
A; Acces A; Statu A; Molec	ssion: F90696 is: preliminary sule type: DNA
A; Resid A; Cross A; Exper C; Genet A; Gene	A;Residues: 1-5291 «TAX> A;Cross-references: UNIPROT:Q8X2T1; GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:G A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: BCs0542
Query Ma Best Loc Matches	/ Match 3.7%; Score 208; DB 2; Length 5291; Local Similarity 20.6%; Pred. No. 0.021; Nes 173; Conservative 114; Mismatches 319; Indels 234; Gaps 34;
δ	GAFNSSVGDSPAVPAETO
qa	2854 GSDLAL-SGTSDQPAGTAITVTLNGQNYSATTDASGNWSVTVPASAVSALGEATY 2907
ò	250 KEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVIVEKSPVLTVTPGSTEHSIPTPPT 309
qq	TASHNVQVNTALPGITINPVATDDI
ò	310 SAAPSESTPSELPISPITAPRIVKELIVSAGDNLIIILPDNEVELKAFVA 359
Ор	2964 GAAAGSTVTVELGGKTYTÄTVQADLSWNVSVPAADWQALGNGELTVNASVTNA 3016
ò	
q	
ò	OLOELT 
đ	3074 VINNQTYAATVLANGSWSVGVPATDVSNWPAGTLNITVSGANSAG-TQTSITHPLT 3128
ò	LPLTSALIDGSQSTDDEING
g	3129 VDLTAVAISMNSITSDDAINAAEKGAALTLSGSTSGVEAGQTVTVTFGGKTYTTTVAANG 3188
ò	476 PFIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAV 525
QQ	VRVI
È	526 DYPPVANAGPNHTITLPONSITLNGNQSSDDHQIVLYEWSLGPGSEG 572
qq	3242 ASDNIINASEAAAGVTVSGTSTAQTGQTLTVTLNGTNYQTTVQTDGSWSL 3291

. 629 Db 374 IETPDXYYKLVIRPTQRSDSGEYLVTATNTSGKDSVLVNVVITDKPSNG 424	3341 Qy 441 684 Db 425	3401 Qy 496 733 Db 484	1452   Qy   553 SSDDH	847 Db 590 FRVSAVNAAGTGEPSDSTPPIIAKARNKPPIIDRSSLVEVRIKAGQSFTFDCKVSGEPAP 3542 Qy 594DYTFQLKVTDSSRQOSTAXVTV	886 Db 650 QTKWLLKKKEVYSKDNVKVTNVDYNTKLKNSATRSDSGIYTVFRENANGEDSADVKVTV 3602 QY 616 IVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENID	Db 710 IDKPAPPNGPLKVDEINSESCTLHWNPPDDDGGQPID 746  Qy 676 KAIATVTGLQVGTYHFRLTVKDQGLSSTSTLTVAV 711	Qy 767 IDGSDHSVALQLTNLVEGV-YTFHLRVTDSQGASDTDTAT 805	RESULT 5 B85547 probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7 C, Species: Escherichia coli C, Species: Escherichia coli C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C; Accession: B85547	48; 132 171 192	192 234 242	VEK 289 Query Match 3.6%; Score 203.5; DB 2; Length 5188; Best Local Similarity 20.8%; Pred. No. 0.036; Matches 165; Conservative 109; Mismatches 296; Indels 223; Gaps 33;	Qy	HKQT 392  QY 250 KEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPT 309
KHVVMGGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVA	-TLPASDLTALANNGYTLTATVSDLAGNLGSASKGVTVDTTAPVISFNTVA -KELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGL		AGIVTISAȚITDSAGNSSTQTHNVQVNTAAVSLSVSTISGDHLINAEAG	SF-F	LDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKV-LKAABVA  VQSRPPFKV-LKAABVA  VQSRPPFKV-LKAABVA	change 09-	97.002.	I ?	187; Conservative 99; Mismatches 258; Indels 410; Gaps 80 VSCPHKENCEPKKMGPIRSYLIFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGD	OODPELHYLNESASTPA-PKLPERSVV :	TPSSGEVLE-KEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEK	SPVLTV	KELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQCHKQT :: : :

g	:             2964 GAAAGSTVTVELGGKTYTATVQADLSWNVSVPAADWQALGNGELTVNASVTNA 3016	ò	99 YLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRKDL 141
à	360 PAPPVETTYNYE-WNLISHPTDYQGEIKQG 388	q	2468 YTKLVIRPPQRTDSGEYLVTATNTSGKDSVLVNVVITDKPSPPNGPLQISDVHKEG 2523
a D	3017 VGNTGSGTRDITIDASLPGLRVDTVAGDDVVNIIEHAQAQVITGSSSGFAAGTALTV 3073	ò	110
È	389HKQTLNILSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVSPQLQELT 446	qq	2524 CHLKWKRPSHDGGTPIEYFQIDKLEPETGCWIPSCRSTAPQVDVTGLSPGNE 2575
q <sub>0</sub>	3074 VINNQTYAATVLANGSWSVGVPATDVSNWPAGTLNITVSGANSAG-TQTSITHPLT 3128	ò	193 GAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTT 241
ý	447 LPLTSALIDGSQSTDDEING 475	qq	2576 YKFRVŠAVNAEGESQPLVGDESIVARNPFDEPGKPENLKATDWDKDHVDL 2625
a	:   :   :     3129 VDLTAVAISMNSITSDDAINAAEKGAALTLSGSTSGVEAGQIVTVTFGGKTYTTTVAANG 3188	λõ	242PSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKS 290
à	NLDPGNYSFRLTVTDS	qq	2626 AWTPPVIDGGSPISCYIIEKQDKYGKWERALDVPADQCKATIPDLVEGQTYKF 2678
q	3189 SWSTTVPAADLAALRDGDASAQVRVTNVNGNSATATHEXSVDSAAPTVTINTI 3241	ò	291 PVLTVTPGSTEHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNL 343
ò	526 DYPPVANAGPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGPGSEG 572	qa	2679 RVSAVNAAGTGEPSDSTPPIIAKARNKPPIIDRSSLVEVRIKAGQSF 2725
q	3242 ASDNIINASEAAAGUTVSGTSTAQTGQTLTVTLNGTNYQTTVGTDGSWSL 3291	ò	344 IITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQ 397
ò	573 KHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVA 629	QQ	2726 TFSATR 2772
д	3292TLPASDLTALANNGYTLTATVSDLAGNLGSASKGVTVDTTAPVISFNTVA 3341	č	398 LSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVSPQLQELTLPLT 450
ò	630 GPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGL 684	QQ	2773 SDSGIYTVFAENANGEDSADVKVTVIDKPAPPNGPLKVDEINSESCTLHWN 2823
a a	3342 GDDVINNVEHIQAQIISGTATGAVAGDRLVVTIAGQQYVTSTDASGNWSVGVPASVISGL 3401	ò	451 SALIDGSQSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGN-YSFRLTVTD 507
à	685 QVGTYHFRLIVKDQQGLSSTSTLIVAVKKENNSPPRARAGGRHVLVLPN 733	qq	-TAGETDGPVTAL
qq	3402 ADGTVIISATITDSAGNSTQTHNVQVNTAAVSLSVSTISGDNLINAAEAG 3452	ò	TTAALIVNNAVDYPPVANAGPNHTITLPQNSIT
à.	g.	q <sub>Q</sub>	2881 RQGTSEPLTTAQAITAKNPFDVPTKP-GTPTIKDFDKEFVDLEWT 2924
q	3453 SALTLSGTGTNFATGTV7TVLLNGKGYSATIQSNGSWSVNVXAA 3496	ò	566 LGPGSEGKHVVMQGVQTPYLHLSAMQEG-DYTFQLKVTDSS- 605
ò	778 -LINLVEGV-YTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQY-GVGQL-TEQR 833	qq	2925 RPEADGGSPITGYVVEKRDKFSPDWEKCABISDDITIAHVPDLIEGLKYEFRVRAVNKAG 2984
qq	3497 DVAALSDGTSYTVSASAQDSAGNSATASRSVAVDLTAPVISINTVSTDDR 3546	ò	606 -RQSTAXVIVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGI 655
à	834 KDTLVRQLAVLIN 846	QQ	2985 PGSPSDATETHVARPKIPPKIDRNFMSDIKIKAGNVFERDVPVTGEPLPSKD 3037
qq	3547 XNAAEQQQPLTIN 3559	ò	656 VFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQOGLSSTSTL 707
# # # # # # # # # # # # # # # # # # # #		qq	3038WTHEGNMIINTDRVKISNFDDRTKIRİLSAİS-DTGVXTLTARNINGTDRHNVK 3090
T13931	o in - fruit flv (Drogonhila melanodagter) (fradment)	ò	708 TVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWI 755
C; Spec.	Sophila melanogaster -1999 #sequence revision 20-Sep-19	QΩ	AMRWV
C, Acce. R, Daley	C,Accession: T13931 R,Daley, J.; Southgate, R.; Ayme-Southgate, A.	ò	
J. Mol	279, 2	q	3146PVGDCTDTEIRADNLIENHDYSFRVRAVNKQGQSQPLTTSQPITAKDPY 3194
A;Refe	8300339; PMID:9636710	ò	809 - QPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVI 867
A; Stati	Secon: 113531 us: preliminary; translated from GB/EMBL/DDBJ	ΩP	3195 SHPDKPĠQPQATDWGKHFVDLEWSTPKRDGGAPIŚSYI 3232
A;Resi	A;NOSCOLE CYPE: DAR A;Roscidues: 1-6658 ADAL> A:Crosc-references: INIPROT:076281: FMRL:AF047475: NID:03337430: PID:03337431: PIDN:AAC2	ò	868 VFYVQSRPPFKVLKAAEV 885
C; General		д	3233IEKRPKFGQWERAAV 3247
A;Cros		RESULT	7
A;Note: int: C;Keywords:	: intron positions not resolved (incomplete sequence) ords: muscle	AC1018 large r C:Speci	AC1018 large repetitive protein [imported] - Salmonella enterica subsp. enterica serovar Typhi C.Snecies: Salmonella enterica subsp. enterica serovar Typhi
Quer Best Matcl	Query Match 3.6%; Score 202.5; DB 2; Length 6658; Best Local Similarity 21.7%; Pred. No. 0.059; Matches 199; Conservative 109; Mismatches 341; Indels 269; Gaps 53;	A; Note: C; Date: C; Acces	A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AC1018

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G6483

hypothetical protein MJ1468 - Methanococcus jannaschii
Cispeciaes: Methanococcus jannaschii
Cispeciaes: Methanococcus jannaschii
Cispeciaes: Methanococcus jannaschii
Cipate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Ju1-2004
C;Accession: C64483 #sequence_Tevision 13-Sep-1996 #text_change 09-Ju1-2004
C;Accession: C64483 #sequence_Tevision III Fleischmann, R.D.; Sutton, G.G.; Blake, R.Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Fren, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A; Reference number: ABO502; MUID:21534947; PMID:11677608
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-3283 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD09244.1; PID:g16505248; GSPDB:GN00176
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Cispecies: VCA0027 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 TYDFYGGWNNVLGHQTALYCGSFMRPGQCDGKGVDENGEPYKGPAYTTDNGIQLLLAQGV
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23.8%; Pred. No. 0.0038;
tive 67; Mismatches 187; Indels 105;
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A;Map position: 2
C;Superfamily: chitinase with C-terminal chitin-binding domain
     3192 ADGSYTFTVTVTDVAG 3207
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Best Local Similarity 23.8*
Matches 112; Conservative
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A;Gene: bca
C;Keywords: tandem repeat
F;207-308/Region: 82-residue tandem repeat
F;309-390/Region: 82-residue tandem repeat
F;304-372/Region: 82-residue tandem repeat
F;355-636/Region: 82-residue tandem repeat
F;555-636/Region: 82-residue tandem repeat
F;637-718/Region: 82-residue tandem repeat
F;637-718/Region: 82-residue tandem repeat
F;819-800/Region: 82-residue tandem repeat
F;801-882/Region: 82-residue tandem repeat
F;833-964/Region: 11-residue partial tandem repeat
F;997-1014/Domain: transmembrane #status predicted <TRM>
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Best Local Simi
Matches 173;
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A46405
C procion alpha antigen - Streptococcus sp. (strain A909, group B, type Ic)
C; precies: Streptococcus sp.
C; paccession: A46405; B46405; T30864
C; paccession: A46405; B46405; T30864
R; Michel, J.L.; Madoff, L.C.; Olson, K.; Kling, D.E.; Kasper, D.L.; Ausubel, F.M.
R; Michel, J.L.; Aadoff, L.C.; Olson, K.; Kling, D.E.; Kasper, D.L.; Ausubel, F.M.
A; Title: Large, identical, tandem repeating units in the C protein alpha antigen gene, b
A; Accession: A46405
A; Molecule type: DNA
A; Recidues: 1-1020 cMIC>
A; Cross-references: GB:M97256; NID:g153558; PIDN:AAA26848:1; PID:g153559
A; Orces: sequence extracted from NCBI backbone (NCBIN:117590, NCBIN:117593)
A; Note: the source is designated as Streptococcus agalactiae, group B, strain A909; ATCC
C; Genetics:
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: C64483
A;Actessive: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-1009 <BUL>
A;Residues: 1-1009 <BUL>
A;Residues: UNIPROT:Q58863; GB:U67587; GB:L77117; NID:g1592103; PID:g1592109; TI A;Map position: POR1437031-14440060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGATNSTTAALIVNNAVDYPPVA-----NAGPNHTITLPQNSITLNGNQSSDDHQIVL 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---DFGDGTPANTTTNPIIIHKYKKEGVYP 954
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hypothetical protein K06A9.1a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-0ct-1999 #text_change 09-Jul-2004
C;Accession: T34A3
R;Geisel, C.; Gattung, S.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid K06A9.
A;Reference number: Z21525
A;Accession: T34A34
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T34A34
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: UNIPROT: Q8IEX6; EMBL: U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:KG
A;Experimental source: strain Bristol N2; clone K06A9
C;Genetics:
A;Gene: CSSP:K06A9.1a
A;Gene: CSSP:K06A9.1a
A;Gene: CSSP:K06A9.1a
A;Map position: X
A;Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2045/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1030 -----TIGSSQG--STSPVVSTISQGSTETPGSTGS---TVTKPS---TVSG 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1069 SASSGSTATMG-----STEASSTSGGSSTS-----PNPSQSTSPSTSGATSSPGSS- 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     800
                                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 LPTTPSS------GEVLEKE---KASQLQEQSSNSSGKEVLMPS-HSLPPASLE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    642 EGSTASSPTGSTGSTFSVATEVTSQSTVPSGSSLGTQSTNSS-----PSPSSLSPSTSG 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 LSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGD 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           696 MSTLTSEPSPSSTQSSGA-QSTLTTP--SPNPSQSTSS---LESSTSGAT----TSSGSA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 DDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALI 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNNAVDYPPVANAGPNHTIT----LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVV 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               577 MQG-VQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXV-----TVIVQPENNRPPVAV 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             927 SÓGSTÓTP----GSTGSTVTÓPSTVSDSTSSGSTVTVGSTEGSSSPIPSTSONTNPSTS 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629 AG-----PDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIAT 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       746 GTTMTSPSQSSSVGSSQGSTSPAASTTS-----GEMTSQGSTQTPG-SSVST 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        792 SAAILTSTQQSVS----STVSGSTVTRP----STVSGSTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLINLVEGVYTFHLRVTDSQGASD
                                                                                                                                                                                                                                                                                                                                                                                                 189 PGSEGAFNSSVGDSPA-----VPAETQQDPELHYLNESASTPAPKLPERSVLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                 584 PGSSSTVPSSSSPQPSSQSPAPNTGSTTPSQTSSQSPSPSMVPSSSTPTGS--SQSTITP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEI-KQGHKQTLNLSQLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           825 GSTVTVGSTEASTSGSSVASSSPAPS---TSQNPNPSTSSGSSMITQSPYPSQSTSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              879 VESSTTPSP---GSPGTTLTSTSPSPSQSTTIGSTQGST----SPGISTTSEEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681 VTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDG
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                Indels 185;
                                                                                                                                                                                                                                                                                                                               DB 2; Length 2232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDTATVEVQPDPRKS-----GLVELTLQVGVGQLTEQ 832
                                                                                                                                                                                                                                                                                                                               Query Match 3.5%; Score 195.5; DB 2; Best Local Similarity 21.7%; Pred. No. 0.029; Matches 152; Conservative 75; Mismatches 287;
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RESULT 12

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Cipecies: Oryctolagus cuniculus (domestic rabbit)
Cipacies: Oryctolagus cuniculus (domestic rabbit)
Cipacies: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
Cipacession: 146521
Kilabeit, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U.;
Nature 345, 273-276, 1990
A;Title: A regular pattern of two types of 100-residue motif in the sequence of titin.
A;Reference number: 146520; MUID:90238553; PMID:2129545
A;Accession: 146520; MUID:90238553; PMID:2129545
A;Accession: 146521
A;Accession: 146521
A;Accession: 146520
A;Accession: 146520
A;Accession: Interpretation of two types of 100-residue motif in the sequence of titin.
A;Reference number: 146520; MUID:9023853; PMID:2129545
A;Accession: 146520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QLQEQSSNSSGKEV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EHSIPTPPTSAAP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 SAPŠESTGTIICKDEYEAPTIVLDPTIKDGLTIKAGDTIVLNAISILGKPLPKSSWSKAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 SESTPS---ELPISPTTAPRTVK-----BLTVSA-----GDNLIITL-----PDN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TTYNYEWNLISHPTDYQG-----E 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385 IKOGHKOTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNL--PPVAVVSPQL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QELTLPLTSALIDGSQSTDD--TEIVSYHWEEINGPFIE----EKTSVDSPVLRLSNLDP 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-----DHOIVLYE-W---SLGPGSEGKHVVMQGVQTP---YLHLSAMQEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SSVGDSPAVPAE--TQQDPELHYLNESASTPAPKLPE----RSVLLPLPTTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 YLVSCPHKENC-EPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 IRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.4%; Score 192.5; DB 2;
larity 19.8%; Pred. No. 0.013;
Conservative 134; Mismatches 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMPSHSLPP--ASLELSSVTVEKSPV---LTVTPGST--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSSRQQSTAXVIVIVQPENNR--
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8 & 8	### ##################################	g & g	801 TGAQAGDIVTVTLANVDYTTVVUGSGNWSLGVPASVVSGLADGSTF 846 691 FRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIV 750 1:-  - - - - - - - - - - -
ò 5	HSVALQLINLVEG-VYTFHLRVTD	ે દ	751 SYLWIRDGQSPAAGDVIDGSDHSVALQLINLVEGVYTFHLRVIDSQGASDTDIATVEVQ 809
}	SQGAS 799	3	
ą	973 SAGRS 977	RESULT 14 A85547 hypotheti	4 dical protein 20609 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
RESULT E90696 hypothe C;Speci	13 tical protein ECs0541 [imported] - Escherichia coli (strain O157:H7, substrain RI es: Escherichia coli 18.11.12001 Heammone ravision 18.11.12001 #Feart change 00.11.12004	C;Specie C;Date: C;Access R;Perna, iller, L	C;Species: Bscherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: A65547 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
C; Accer R; Hayar gasawar	C;Accession: B90696 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	A, Title: A, Refere A, Access	Genome sequence of enterohemorrhagic Escherichia coli O157:H7. ace number: A85480; MUID:21074935; PMID:11206551
DINA KEI A;Titl( A;Refer A;Acces A;Statu	DNA KES. 8, 11-22, 2001 A;File: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: E90696 A;Status: preliminary	A;Status A;Molecu A;Residu A;Cross- A;Experi	: prefinitionry 81 Lype: DNA 82 1-1461 <sto> references: UNIPROT:QBXD19; GB:AE005174; NID:g12513364; PIDN:AAG54837.1; GSPDB:G mental source: strain O157:H7, substrain EDL933</sto>
A, Molec	ule type: DNA hues: 1-1461 - HNY- nues: 1-1401 - HTD - 11150000 GOUND COURTY BENEVIATION OF THE STATE OF THE	C,Geneti A,Gene:	6090Z
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Querj Best Matc}	Query Match 3.4%; Score 190.5; DB 2; Length 1461; Best Local Similarity 21.1%; Pred. No. 0.029; Matches 139; Conservative 81; Mismatches 214; Indels 225; Gaps 28;	% <del>Q</del>	191 SEGAFNSSYGDSPAVPAETQQDPELHYLNESASTPAPKLPERSYLLPLPTTPSSGEVL 248
ờ සි	191 SEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVL 248	ර සි	249 EKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEH 302 i.
<u>ک</u> ۾	249 EKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEH 302 487 NNAEOAVALISGOVSGSPGDTVTVK.GTHVLTGTVLADGSMNVALDPATRTLDRGAN 546	ඊ සි	303 SIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFV 358
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<i>&amp;</i> 7	APAPPVETTYNYEWNLISHPTDYQGEIKQCHKQTLANLSQLSVGLYVFKVTVSSENAFGEG	8 8	FVNVTVKPARRVNLPPVAVVSPQLQBLTLPLTSALIDGSQSTDDTBIVSYHWEBINGPF1
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රු සි	534 GPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEG 593	& <del>8</del>	594 DYTRQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATL 644 :
ò	DYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATL	ò	645 DGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYH 690
QQ	744 NATVTASVNDVAGNPSSVSRVALVDATPPVVTINPVATDNVINTPEHAQAQIISGTV 800	Db	DYTTVVDGSGNWSLGVPASVVSGLADG
ò	645 DGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYH 690	ò	691 FRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIV 750

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